

CDS
 1651. 2817
 /gene="SCIA9.03"
 /note="SCIA9.03, probable two component sensor kinase, len: 388aa; similar to a family of sensor kinases eg. TR:053893 (EMBL:U51332) AbsA1 from Streptomyces coelicolor (571 aa), (fasta scores: opt:.389, z-score: 278, E): 2.9e-08, 33.1% identity in 405 aa overlap) and UPR_FCOLL (EMBL:M17102) sensor kinase from Escherichia coli (500 aa), (fasta scores: opt:221, z-score: 248.0, E): 1.5e-06, (25.9% identity in 398 aa overlap). Contains several possible membrane spanning domains."
 /codon_start=1
 /transl_table=1
 /product="putative sensor kinase"
 /protein_id="CA22373.1"
 /db_xref="GI:4007688"
 /translation="MIDRRVLELMRRLDVVRDLPLGLVLLASLPSLGSGTEITGGLPIRPALAGVAVALOSIPLAVRRHTLLCLTVSGFALDOLRAVHIFAGALGPIVLINAGSQEYRRRTQYATLGYVAAVGLNARGSDTELYETFTYVLLANGICNWMRSRAAEARSRVADNARNARETIRLRLHGVTHVTHVADLVQSEAAATYLAAPERFLDESLAVSDTGRALITDLNLHLDLPNDIPDIEPRPPRGVRLTVEQYRRAGPQEFTEGCTPAATSGSDLVAVRVQDALNLAKYHGHTVSLVRHGEETIIVEGTGGSGSAASGSGSGRLAGLRERVDYLGGEFTDRADGGEVVARIPGSGSGTA"
 2814. 3473
 /gene="SCIA9.04"
 2814. 3473
 /gene="SCIA9.04"
 /note="SCIA9.04, probable luxR family response regulator, len: 219 aa; similar to a family of regulators eg. TR:069816 (EMBL:AL023496) probable two component regulator from Streptomyces coelicolor (224 aa) fasta scores: opt:714, z-score:1103.5, E():0. (54.48 identity in 219 aa overlap) and NARL_ECOLI (EMBL:X13360) nitrate/nitrite response regulator from Escherichia coli (216 aa) fasta scores: opt: 465, z-score: 656.5, E(): 2.7e-29, (37.6% identity in 213 aa overlap). Contains Pfam match to entry PF00072 response_reg, Response regulator-receiver domain, score 111.10, E-value 2.1e-29, Pfam match to entry PF00196 GERE, Bacterial regulatory proteins, luxR family, score 79.50, E-value 7e-20, PS00622 Bacterial regulatory proteins, luxR family signature and an helix-turn-helix motif from: 1 to: 219, Score 983 (+2.53 SD)."
 /codon_start=1
 /transl_table=1
 /product="putative response regulator"
 /protein_id="CA22374.1"
 /db_xref="GI:4007689"
 /translation="MSAFIRYICDDDAALITFGATLYADQADLVQSEGCCDGTGVDLARELRPQVVMQIRMPVLDGLFETRLLAGGVAAHPKVALVTFNIDEEYVLAIRGASGFLKMAPDRLGLIRIVAMGAALIDPVTVRRLVQVRARIRPEGTRADIPLRPQRETRELRLKADGENSEIALVALVISPETVKFTVSRIITKLDRDQVAVVPRHGLV"
 2826. 3173
 /gene="SCIA9.04"
 /note="Pfam match to entry PF00072 response_reg, Response regulator receiver domain, score 111.10, E-value 2.1e-29"
 3276. 3470
 /gene="SCIA9.04"
 /note="Pfam match to entry PF00196 GERE, Bacterial regulatory proteins, luxR family, score 79.50, E-value 7e-20"
 3327. 3410
 /gene="SCIA9.04"
 /note="PS00622 Bacterial regulatory proteins, luxR family signature."
 complement(3492. 4094)
 /gene="SCIA9.05c"
 complement(3492. 4094)
 /gene="SCIA9.05c"
 /note="SCIA9.05c, possible transmembrane protein, len: 200 aa; contains possible membrane spanning hydrophobic regions"
 /codon_start=1
 misc_feature
 2826. 3173
 /gene="SCIA9.04"
 /note="Pfam match to entry PF00072 response_reg, Response regulator receiver domain, score 111.10, E-value 2.1e-29"
 3276. 3470
 /gene="SCIA9.04"
 /note="Pfam match to entry PF00196 GERE, Bacterial regulatory proteins, luxR family, score 79.50, E-value 7e-20"
 3327. 3410
 /gene="SCIA9.04"
 /note="PS00622 Bacterial regulatory proteins, luxR family signature."
 complement(3492. 4094)
 /gene="SCIA9.05c"
 complement(3492. 4094)
 /gene="SCIA9.05c"
 /note="SCIA9.05c, possible transmembrane protein, len: 200 aa; contains possible membrane spanning hydrophobic regions"
 /codon_start=1
 misc_feature
 2826. 3173
 /gene="SCIA9.04"
 /note="Pfam match to entry PF00072 response_reg, Response regulator receiver domain, score 111.10, E-value 2.1e-29"
 3276. 3470
 /gene="SCIA9.04"
 /note="Pfam match to entry PF00196 GERE, Bacterial regulatory proteins, luxR family, score 79.50, E-value 7e-20"
 3327. 3410
 /gene="SCIA9.04"
 /note="PS00622 Bacterial regulatory proteins, luxR family signature."
 complement(3492. 4094)
 /gene="SCIA9.05c"
 complement(3492. 4094)
 /gene="SCIA9.05c"
 /note="SCIA9.05c, possible transmembrane protein, len: 200 aa; contains possible membrane spanning hydrophobic regions"
 /codon_start=1
 misc_feature
 2826. 3173
 /gene="SCIA9.04"
 /note="Pfam match to entry PF00072 response_reg, Response regulator receiver domain, score 111.10, E-value 2.1e-29"
 3276. 3470
 /gene="SCIA9.04"
 /note="Pfam match to entry PF00196 GERE, Bacterial regulatory proteins, luxR family, score 79.50, E-value 7e-20"
 3327. 3410
 /gene="SCIA9.04"
 /note="PS00622 Bacterial regulatory proteins, luxR family signature."
 complement(3492. 4094)
 /gene="SCIA9.05c"
 complement(3492. 4094)
 /gene="SCIA9.05c"
 /note="SCIA9.05c, possible transmembrane protein, len: 200 aa; contains possible membrane spanning hydrophobic regions"
 /codon_start=1
 misc_feature
 2826. 3173
 /gene="SCIA9.04"
 /note="Pfam match to entry PF00072 response_reg, Response regulator receiver domain, score 111.10, E-value 2.1e-29"
 3276. 3470
 /gene="SCIA9.04"
 /note="Pfam match to entry PF00196 GERE, Bacterial regulatory proteins, luxR family, score 79.50, E-value 7e-20"
 3327. 3410
 /gene="SCIA9.04"
 /note="PS00622 Bacterial regulatory proteins, luxR family signature."
 complement(3492. 4094)
 /gene="SCIA9.05c"
 complement(3492. 4094)
 /gene="SCIA9.05c"
 /note="SCIA9.05c, possible transmembrane protein, len: 200 aa; contains possible membrane spanning hydrophobic regions"
 /codon_start=1
 misc_feature
 2826. 3173
 /gene="SCIA9.04"
 /note="Pfam match to entry PF00072 response_reg, Response regulator receiver domain, score 111.10, E-value 2.1e-29"
 3276. 3470
 /gene="SCIA9.04"
 /note="Pfam match to entry PF00196 GERE, Bacterial regulatory proteins, luxR family, score 79.50, E-value 7e-20"
 3327. 3410
 /gene="SCIA9.04"
 /note="PS00622 Bacterial regulatory proteins, luxR family signature."
 complement(3492. 4094)
 /gene="SCIA9.05c"
 complement(3492. 4094)
 /gene="SCIA9.05c"
 /note="SCIA9.05c, possible transmembrane protein, len: 200 aa; contains possible membrane spanning hydrophobic regions"
 /codon_start=1
 misc_feature
 2826. 3173
 /gene="SCIA9.04"
 /note="Pfam match to entry PF00072 response_reg, Response regulator receiver domain, score 111.10, E-value 2.1e-29"
 3276. 3470
 /gene="SCIA9.04"
 /note="Pfam match to entry PF00196 GERE, Bacterial regulatory proteins, luxR family, score 79.50, E-value 7e-20"
 3327. 3410
 /gene="SCIA9.04"
 /note="PS00622 Bacterial regulatory proteins, luxR family signature."
 complement(3492. 4094)
 /gene="SCIA9.05c"
 complement(3492. 4094)
 /gene="SCIA9.05c"
 /note="SCIA9.05c, possible transmembrane protein, len: 200 aa; contains possible membrane spanning hydrophobic regions"
 /codon_start=1
 misc_feature
 2826. 3173
 /gene="SCIA9.04"
 /note="Pfam match to entry PF00072 response_reg, Response regulator receiver domain, score 111.10, E-value 2.1e-29"
 3276. 3470
 /gene="SCIA9.04"
 /note="Pfam match to entry PF00196 GERE, Bacterial regulatory proteins, luxR family, score 79.50, E-value 7e-20"
 3327. 3410
 /gene="SCIA9.04"
 /note="PS00622 Bacterial regulatory proteins, luxR family signature."
 complement(3492. 4094)
 /gene="SCIA9.05c"
 complement(3492. 4094)
 /gene="SCIA9.05c"
 /note="SCIA9.05c, possible transmembrane protein, len: 200 aa; contains possible membrane spanning hydrophobic regions"
 /codon_start=1
 misc_feature
 2826. 3173
 /gene="SCIA9.04"
 /note="Pfam match to entry PF00072 response_reg, Response regulator receiver domain, score 111.10, E-value 2.1e-29"
 3276. 3470
 /gene="SCIA9.04"
 /note="Pfam match to entry PF00196 GERE, Bacterial regulatory proteins, luxR family, score 79.50, E-value 7e-20"
 3327. 3410
 /gene="SCIA9.04"
 /note="PS00622 Bacterial regulatory proteins, luxR family signature."
 complement(3492. 4094)
 /gene="SCIA9.05c"
 complement(3492. 4094)
 /gene="SCIA9.05c"
 /note="SCIA9.05c, possible transmembrane protein, len: 200 aa; contains possible membrane spanning hydrophobic regions"
 /codon_start=1
 misc_feature
 2826. 3173
 /gene="SCIA9.04"
 /note="Pfam match to entry PF00072 response_reg, Response regulator receiver domain, score 111.10, E-value 2.1e-29"
 3276. 3470
 /gene="SCIA9.04"
 /note="Pfam match to entry PF00196 GERE, Bacterial

	Query Match	Best Local Similarity	Matches	24.6%	Score 532.4	DB 29	Length 29400	
				58.0%	Pred. No. 9.8e-131	Mismatches 726	Indels 12	Gaps 4
gene	CD5	transl_table=1 /product="putative transmembrane protein" /protein_id="CA422375.1" /db_xref="GI:4007690" /translation="MFRAANGIRSAPIVHVEPMKDNASTERSDRPRLRRSLMGIGVALLAGVAVRLNCTSAWLSALLCAVPAALVIVMVRRLRDRAVCAEEDDPAAMEEOLIKGGPAPDRPDRMAAFVFSRDSRRAVRRMWRAPMLAVIFFGISALMYLTS GSGVGSIMGLGIVFLGMLAWMYLRLDRLSHRGLRG"	4140..4631 /gene="SC1A9..06" 4140..4631 /gene="SC1A9..06"					
QY	332	acacagctacgcagacagacattatctgacatttgaagctcaagctcgaatgctgacatca	391					
Db	18101	ACAGAGCTCCCGGAGACAGTTCGTGACATCTCAACCCCGCGGGGTGACAGCCCTCTA	18160					
QY	392	tggtttggtggtgacagcttaacgcgatcgttgatgctgct--ccgccaatcagatat	448					
Db	18161	CGGAGTCTCTCGGGGACACCTCAACCCCGTGTGACACCCGCGCCGACATTCGGGAT	18220					
QY	449	tgaagtgtgacgtctgaaatgagaaagcgagcgctttgacagcgtctgagatgct	508					
Db	18221	CGAATGGGTGACGTACCGGACGAGAAACCGCCCTTCGCGCGGCGGAGGCGCA	18280					
QY	509	gatacctggtgagatgctgacatgctgctctctgtgctcgtgaaacacacatgctat	568					
Db	18281	GATCACCGGAGAGTCAACCGGCGGCGGCGGCTCTCGCGCCCGCCGACATCTACATCAT	18340					
QY	569	tcaggtgtcttaatgattcgaatcgaatgctgagaaagtgctgagaaagtgctgacat	628					
Db	18341	CAACGGGCTCTACGACGCGCCACCGCTCCATGAGCCCGCTCTCGGCTCCAGAT	18400					
QY	629	tcgagatgcccagatgtgttcgaagctttcttcagaaacgataccgagatttgttaa	688					
Db	18401	CCCTGCCAGCAGATCGGGCTCGGCTTCTTCAGAGAACCCACCCGACACACTTTCG	18460					
QY	689	gnaatgtctgttactgtactgtgagatggtgaaatggtgtgagcaggttgaaacatttga	748					
Db	18461	CGAGTGCAGTCACTACAGCAGAGCTGATCTCCAGCCCGAAGCAGAGTCCCGGCTCTCA	18520					
QY	749	tcaagcgatctaatgacccaatgctgagcggttaaggtgtgtcgtgtgtgtgtgtatc	808					
Db	18521	GACCGCCTTCCAAACACCGCGCTCGGCGACGGCGGCTTCAGCGTCTGCTCCCGGCA	18580					
QY	809	tatcgtaagaaagcagagtgaaagtgactatttcaaatccaaattcttcttcgagac	868					
Db	18581	CATGCGGACAGACGCGCGCGGCGGAGGGGCGCGGACGCGCCCTCTGACCTCCGGCC	18640					
QY	869	tcctgtgtgttctcccgatcttactactgaagctctgacgctgtgtgtgagcgtgaaacagc	928					
Db	18641	CACGCTCGG---CCGCGCGACAGAGATGACACGCGGCTGCGGATGATGACGAGCGC	18697					
QY	929	taagtgtcaacttgttctcgtgtgctgagcggtgaagaatgctcgcgcgcaggtgttga	988					
Db	18698	CGACAAGGTGACCCCTGTTCTCCGACGCGGACCCCGGCGCGCACCGCGAGATATGGA	18757					
QY	989	gttgcgcgaagaagatlaaatcacgaatcgggcacatcgctgtgtgtgtgtgtgtgtgtgt	1048					
Db	18758	GTTGCGCGGGAAGCTCAAGGACACCGTGGGGGCGCGCCCTCGGGGCAAGAGATTATCCA	18817					
QY	1049	gcatatgaagatccgctttgagctgcgcacatgctcgtcgtctgttgaatcggcgcctgcgtga	1108					
Db	18818	GTAGACACAACCCGTAACGACGTGCGCATGAGCGAGATCTCTCGGCTACGCGCGCGCTACGA	18877					
QY	1109	tgcgtccaatgaagcgcgtctgctgtgattctatctgtgtgtgtgtgtgtgtgtgtgtgtgt	1168					
Db	18878	GGCCACCCACAGATGCGACCTGCTCTCTTAATCGGACCCGACATCTCCGTCACACGCTTT	18937					

D	539	TTCCGCAAGTATAGTACACTATTGTGGAGCTGTGTTCCAGCCCGAGCAAGATCCACAAAGTA	598
O	744	ttgcatacgcgcatctcagtlccacaatggcggtaaaagtgctggttgatgtaattcc	803
D	599	CTGGGATTTGGCAATGGCCAAAGGCGTCTTACCGTGGGGTTTCGGTGTTCGTGTACCA	658
O	804	ggtaatacgcataaaggaaagccgaagtgaaagtaactatattcaattccatactcttc	863
D	659	GGCCACCTGGCGTTTAAACACTGGCCAGCAAGAGGGGC---AACCATGCATCGTATCATCG	715
O	864	ggcactccgttgatgtcccggaatccatacgaagctcgaagcgttggtagaagcgaatlaac	923
D	716	CCACACACCAAGTCGTAGCGCCGGAAGAAGAAATTTACGCAACTGGCCGCACTGCTGGT	775
O	924	aacgcataagctctgcaactttgtctcgcgttgccggcgtagaagatgctcgcgcgaagtg	983
D	776	TATTTCAGCAATATTCGCCCTGATGTGTGGCAGCGGTGGCGGGGGCGCATTAAGATTA	835
O	984	cttgagattggsggggaagaaatlaataaccaatcgggcatatgcgttggttgtaagcaatc	1043
D	836	CTTACGTTTCCCGGAAATTTAAAGCGCCTATTGTTCATGCTCCCTGCGCGTAAGAACAT	895
O	1044	atccagcaatgaaatccgcctctgaagtcgcgaatgtcggcgtcgttggttaaggcgcgc	1103
D	896	GTCGAATATACGATATATCCGTATGATGTTGGAAATACCGGGTTAATCGGCTTCTCGTCA	955
O	1104	gtgagatgcgtccaaatgaagcgcgaatctgctgatatctaatctggttaacgaattccctatt	1163
D	956	TTCCATATCCATGATGAAAGCGCGACAGGTTAGTGTCTACTCGGACGCAATTTCCATAC	1015
O	1164	gatttccctccta---aagaacaagttcccaaggatgatatcaacaggatgcacatggt	1220
D	1016	GCCTTTACACCCGACCGATGCCAAATTCATTACATTTGATATACACCAACGACGATCG	1075
O	1221	cgagctacccaagctgtaagatataccggtgaacggatgctgcgcgaacaaatcgaataat	1280
D	1076	GCTACACAGCAAGTGGATATGGCATGTGTGGGATATACGTGACTGTGCGTCAATTG	1135
O	1281	ctgcctcaatgtgaagggaaaaaacagatcgtcttcctctctgatacgaatctcgaagcaac	1340
D	1136	CTTCCATTTGGTGGAAAGAAAGAACCGCATTCGCAATTTCTGGATTAAGCGCTGGAAATTC	1195
O	1341	gaagcgaatgtgagctcgtgtgtgaagaaagctacacacataacgctcgaagaagatgctc	1400
D	1196	CGCGACACCCCAAGAGCGCTGCGACGATTTAGTTAAACCCAGCG-----AGAAAGCC	1248
O	1401	attcaacctgaatacgtctgcctctatatttgaagagccttgccggataaagaatgacgtgt	1466
D	1247	ATTACACCGCAATTTCTGGCGCAGCAAAATTAATGATTTTGGCGCGATGACGCTATTTTC	1306
O	1461	acgttggaataccgcgaatgtgcaatgtgtgcatactgcaatgacatccgaagga	1520
D	1307	ACGTGTACAGTGTGTACGCCAACAGGTGTGTGGCGGCACTTATCT---AATAATGAACGC	1365
O	1521	acgcgcgaacttctggtgtcaatccgcacagcagaatggtcataatgctgtgctctacgc	1580
D	1364	AACGCTGCGCGTTAGCTTCTTTAAACACGCTTCATGGCTAAGCGCATGGCCGACGCG	1423
O	1581	attgtgtgcgaagaatgtgtgtatcgaataaccgcacagtgatctcgatgttggtgcgaatg	1640
D	1424	CTGGGTGCGCAGCGACAGACAGCAAGCAATGCTACAGTGTGTGCTATGTGGCGCATATGG	1433
O	1641	ctgggacatgcctgcctgggttgagactcttcgaacggttaagctcgaacactccgcctgaag	1700
D	1484	TTTAGCATGTGTTGATGGCGGATTTCTCTCATGTAAGTGCAGATTAACACTGCCACTGAATA	1543
O	1701	gtggatgttlaaacaacagatctcttggtgcatactgtagaagctcgttgtagaaggaac	1760
D	1544	GTGCTCTTTTAAACAACACCGTGTGGGGCTTTGTGGCATGTGACATGAAGCTGTGGCTAT	1603
O	1761	ccagaattctgtactgacacatgaagaaatgaaattctgcagagaatctgcgcgcgtctgcgt	1820

Db	1604	TTGACTGACGGACACCGAATCAACAGACACAACAACTTTGCCGCAATTGGCCGAAGCGTGGGC	1653
Qy	1821	atcnaalcgtagtcagcatcacccggtccgaagaagttcgcgagcagctagctgagcaltg	1880
Db	1664	ATTTCGGGTATCCGTGTGAGAAAAAGCGCTGTGAAGTGTGATGAAGCCCTCAACGCCCTTTC	1723
Qy	1881	gcatccctgagacctgtacgcgatcgaatcgcgaagatcctcaatgcgcgtgcgaatccca	1940
Db	1724	TCCATCGACCGTCCCGGTGGTGGATGTGTGGTGTGTCGCCAAGAAGAGTTAACCCTTTCCA	1783
Qy	1941	ccaaccaatcaocgtgagaaacagtcaltggaattcgaagaacgcgcaccgcgaacgcgttctt	2000
Db	1784	CCCGAGATCAACATCGCAACAGGCCCAAGGTTTCAGCCTGTATATCTCTCGCGCATTCATC	1843
Qy	2001	ggtgtagagtagagagatgcgatcgaatgcgtgcgcgcgttcgaac	2042
Db	1844	AGCGGACCGCGTGTGATGAATGATCGAATCGGCCAANAACAAAC	1885

RESULT	3	.
AE000188/c		
LOCUS	AE000188	11429 bp DNA
DEFINITION	<i>Escherichia coli</i> K-12 MG1655 section 78 of 400 of the complete genome.	
ACCESSION	AE000188	U00096
VERSION	AE000188.1	GI:1787084
KEYWORDS		
SOURCE		
ORGANISM	<i>Escherichia coli</i> , <i>Escherichia coli</i>	

REFERENCE
1 (bases 1 to 11429)
AUTHORS
Blattner, F.R., Plunkett, G. III, Bloch, C.A., Perna, N.T., Burland, V.

TITLE
The complete genome sequence of *Escherichia coli* K-12
Science 277 (5331), 1453-1474 (1997)

MEDLINE 9/42061/
 PUBMED 97426617
 REFERENCE 2 (bases 1 to 11429)
 AUTHORS Bialtner, F.R.
 TITLE Direct Submission
 JOURNAL Submitted (16-JAN-1997) Guy Plunkett III, Laboratory of Genetics

University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.
Email: ecollegenetics.wisc.edu Phone: 608-262-2534 Fax:
608-263-7459
3 (bases 1 to 11429)

AUTHORS Blattner, F.R.
TITLE Direct Submission
JOURNAL Summated (02-SEP-1997) Guy Plunkett II, Laboratory of Genetics
University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.
Email: ecoliggenetics.wisc.edu Phone: 608-262-2534 Fax:
608-262-7450

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
4 (bases 1 to 11429)	Plunkett, G., III.	Direct Submission	Submitted (13-OCT-1998)	Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA
				This sequence was determined by the E. coli genome project at

University of Wisconsin-Madison (Frederick R. Blattner, director). Supported by NIH grants HG00301 and HG01428 (from the Human Genome Project and NCHRR). The entire sequence was independently determined from E. coli K-12 strain MG1655. Predicted open reading frames were determined using the GeneMark software, kindly supplied by Mark Borodovsky, Georgia Institute of Technology, Atlanta, GA, 30332 [e-mail: mark@ember.gatech.edu]. Open reading frames that have been correlated with genetic loci are being annotated with CG Site Nos., unique ID nos. for the genes in the E. coli Genetic Stock Center (CGSC) database at Yale University, kindly supplied by Mary Berlyn. A public version of the database is accessible (<http://cgsc.biology.yale.edu>). Annotation of the genome is an ongoing task whose goal is to make the genome sequence more useful

by correlating it with other data. Comments to the authors are appreciated. Updated information will be available at the E. coli Genome Project's World Wide Web site (<http://www.genetics.wisc.edu>). *** The E. coli K-12 sequence and its annotations are periodically updated; this is version M4. No sequence changes. Annotation updates: updated gene identifications and products; all new functional assignments courtesy of Monica Riley; added promoters, protein binding sites, and repeated sequences described in reference 1. The unique numeric identifiers beginning with a lowercase 'b' assigned to each gene (protein- or RNA-encoding) are now designated as gene synonyms instead of labels. This should allow them to be searched for in Entrez as gene names.

FEATURES

source 1. 11429
/organism="Escherichia coli"
/strain="K-12"
/sub_strain="MG1655"
/db_xref="taxon:562"
<1. 15
repeat_region /note="REP (repetitive extragenic palindromic) element; contains 1 REP sequence"
complement(130..861)
/gene="arlJ"
/note="b0860"
complement(130..861)
/gene="arlJ"
CDS /function="transport; Transport of small molecules: Amino acids, amines"
/note="f243; 99 pct identical to ARTJ_ECOLI SW: P30860"
/codon_start=1
/transl_table=1
/product="arginine 3rd transport system periplasmic binding protein"
/protein_id="AAC73947.1"
/db_xref="GI:1787085"
/db_xref="PID:91787085"
/transl_table=1
/translation="MKRLVLAALASFTFGSAAEKINFGVSATYPPESIGANNEIY GFIDILAKLCQMAECTFNHAFDSLIPSLKPRKYDAVSGMDIPERKQVFTT PYENSAIVIAKKDQYKTFADLKGKRGIMGNTYHOKYIODHPEKIVSYDSYNAR IDLKNRGIDVGGDPAVNMELKTNPGVATKENVTDPOYRGTCIGIAVRDNNALLE KLNNAALAIKADGTYOKISDQWFPQ"
promoter /complement(919..947)
/note="factor Sigma70; predicted +1 start at 899849"
1035..1216
repeat_region /note="REP (repetitive extragenic palindromic) element; contains 3 REP sequences"
complement(1152..1820)
/gene="arlM"
/note="b0861"
complement(1152..1820)
CDS /function="transport; Transport of small molecules: Amino acids, amines"
/note="f122; 98 pct identical to ARTM_ECOLI SW: P30862"
/codon_start=1
/transl_table=1
/product="arginine 3rd transport system permease protein"
/protein_id="AAC73948.1"
/db_xref="GI:1787086"
/db_xref="PID:91787086"
/transl_table=1
/translation="MFEYLPMLKGLHSLTLVASLVALIALIFITILTKPVL VMIVRGYITLFTGPIVLQVLIYVGGQFTLQEVPAIMHLISEPMICALIALINS AAYTTOLEYGAIRAIIPGQMOCSAIGMSKKDTAILIILPYAFKRSLSYSSEVVLVFK STSLATYITLMEVNGYSOLYGRYDVAVVEGAAGIITLVNGLITLMKRLTERALAF ERRN"
gene /complement(1820..2536)
/gene="arlQ"
/note="b0862"
complement(1820..2536)
CDS /gene="arlQ"
/function="transport; Transport of small molecules: Amino acids, amines"

/note="f238; 98 pct identical to ARTQ_ECOLI SW: P30861"
/codon_start=1
/transl_table=1
/product="arginine 3rd transport system permease protein"
/protein_id="AAC73949.1"
/db_xref="GI:1787087"
/db_xref="PID:91787087"
/transl_table=1
/translation="MNEFFPLASAGMTGVALCALIVGALAMFAVESAKMRPVA MAGSALVITLGLPEITLVLFIFVGGSQLLTLSDFINLGFVQIIPVQMDIENFVS PELGCVIALSILVAAYASQTLRGALKAAPVGOMESGOALGSKSIFPERLVPMWRH ALPBGONMIVILKDTALVSTISVNDMLQKSTATKROEFTWYAAALTYITLL SQYILKRIDLATRRFRPS"
promoter /complement(1862..1899)
/gene="arlQ"
/note="factor Sigma54; predicted +1 start at 900812"
complement(2199..2216)
/gene="arlQ"
protein_bind /note="central position to predicted promoter: -316"
/bound_molety="Phob predicted site"
complement(2543..3274)
/gene="arlI"
/note="b0863"
complement(2543..3274)
CDS /gene="arlI"
/function="transport; Transport of small molecules: Amino acids, amines"
/note="f243; This 243 aa ORF is 97 pct identical (1 gap) to243 residues of ARTI_ECOLI (244 aa) SW: P30859"
/codon_start=1
/transl_table=1
/product="arginine 3rd transport system periplasmic binding protein"
/protein_id="AAC73950.1"
/db_xref="GI:1787088"
/db_xref="PID:91787088"
/transl_table=1
/translation="MKRLVLAALAGSLSTAAETTRFATASYPPEESIDANNQIV GFVDLAOLCKEIDATCTFSNQAFDSLIPSLKRRVAVAGADITPERKQVLFIT PYVNSALFVGOQKRYTSVDOLKRVGVQGTTHOKIMDKHBEITTVPYDSYNAR LDLONGRIGDVGCTAVVTEMLKDNPKLAAVGDVTDKDYGTGIGIAVRQGNTELQO KLMLALEKVKKDGIVETLYNKWFOK"
gene /complement(3292..4020)
/gene="arlP"
/note="b0864"
complement(3292..4020)
/gene="arlP"
CDS /function="transport; Transport of small molecules: Amino acids, amines"
/note="f242; 98 pct identical to ARTP_ECOLI SW: P30858"
/codon_start=1
/transl_table=1
/product="ATP-binding component of 3rd arginine transport system"
/protein_id="AAC73951.1"
/db_xref="GI:1787089"
/db_xref="PID:91787089"
/transl_table=1
/translation="MSIQNLNGINCFYGAHQALFDITLDCPOGETLVLLGPGSAGKSSL LRVNLLEMPRSGLINAGHFEFTKPSDKAIDLRNVMVQOQNLWMLHLYVOON LIEAPCVLIGLSKQOALARAELKRLKRSYDRPYRLSGGQOORVALARALAMEP QVLLFDEPTALDPEITAOYISITRELAEINIVQYITHEVFAKRTASRVYVENGH IVEQGDASCTFEPQTEAFKNYLSH"
gene /complement(4238..4753)
/gene="ybjp"
/note="b0865"
complement(4238..4753)
/gene="ybjp"
CDS /function="putative enzyme; Not classified"
/note="f171; This 171 aa ORF is 30 pct identical (3 gaps) to 70 residues of an approx. 472 aa protein GLNA_ECOLI SW: P06711"
/codon_start=1
/transl_table=1
/product="putative enzyme"
/protein_id="AAC73952.1"

/db_xref="GI:1787090"
/db_xref="PID:91787090"

Query Match 14.1%; Score 305.2; DB 1; Length 11429;
Best Local Similarity 50.7%; Pred. No. 2, 9e-70;
Matches 873; Conservative 0; Mismatches 828; Indels 21; Gaps 5;

QY 327 atggcaacagcgaacgaacaaatlaattgacatttgaagctcaagtgtaagcga 386
DB 11335 ATGAACAACGCGTTCGATATATGCGCAAAACACTGATCGGAGGGTGAACGC 11276
QY 387 attatagtgcttggttggaagccttaa---tcgactgtagatgctgcgcaatca 443
DB 11275 ATCTGGGGAGTCACAGCGACTCTGMAAGGCTTATGTAACAGTCTTAATCCATGGCG 11216
QY 444 gatattgagtggttggaagcttgcaaaatgaaggaagcgagctttgcaagcttgagaa 503
DB 11215 ACCTATGAGTGTGATGTCACAGCGCGGCTGCGGATCGTGGCGCCGCAACCTGCAC 11096
QY 504 tctgtgacacgttggaagcttggaagcttgctgctcttggtgcttggaacacacac 563
DB 11155 GCACAACTTACGCGAAGACGCGGCTGCGCGGATCGTGGCGCCGCAACCTGCAC 11096
QY 564 ctgactcaaggtcttcaatgactcgcaatgtaggaagtgtagccatcgtagc 623
DB 11095 TTATATACAGGCGCTGTTCGATTCACACGCAATCACGTTCCGCTACTGGGATTCGCGCT 11036
QY 624 catattcgagctgcaagatttgtagaagcttcttcagaagaacgacgcgagatttg 683
DB 11035 CATATTCCTCCAGCAAAATGCGACGCGCTATTTCCAGAAACCCACCAAGACTA 10976
QY 684 tctaaagaatgctctgctgaactgcaagatgtagaagtgtagcagagtgtagcact 743
DB 10975 TTCCGCGAATGTAGTACATATTCGAGCTGTTTCCAGCCCGAGAGATCCCAAGTA 10916
QY 744 tgcatacaagcgaatcaatgcaacacatggaagtgtagtgctgtagtagtact 803
DB 10915 CTGGCGATTTGCGATGCGCAAAAGGCGCTTAAACGTCGCTTTCGTTGCGTTACCA 10856
QY 804 ggtgatactgcaagaagcagtgtagcgtatctcaatctcaatctctctct 863
DB 10855 GGGGAGCTGGCGTTAAACCTGCGCCAGAAAGGCG---AACCATGCACTGTATCATGCG 10799
QY 864 ggcactcctgtagtctcccgatctcaatgagctgtagcagctgtaggaagcgaatca 923
DB 10798 CCACAACTGCTGACCGCGCAAGAAAGAGTACGCAACTGGCGCAACGTCTGCT 10739
QY 924 aagcctaaagctgcaactgctgctgctgctgctgctgctgctgctgctgctgct 983
DB 10738 TATTCAGCAATATCCCGCTGATGTGTGAGCGGCTGCGCGGCGCATTAAGATTTA 10679
QY 984 tggagctgtaggaagaatlaatacgaatcgagcgtgtagtgtaggaagtagc 1043
DB 10678 GTTGAATTTGCGCGAATAATTAAAGCGCTTATGTTATGCTGCGCGGTAAGAACAT 10619
QY 1044 atccagcaatgaatcgtttagagctgtagcagctgctgctgctgctgctgctgctgct 1103
DB 10618 GTTCGATATGATATGCTGATGTTGGAATGACCGGTTAATCGGCTTCTGCTGACGT 10559
QY 1104 gtagatgctgcaatgaagcgagctgctgctgctgctgctgctgctgctgctgct 1163
DB 10558 TTTCATATCATATGTAAGCGCGACAGCTTATGCTACTGCGCGCAATTTCCCTACCGC 10499
QY 1164 gattctctctccta---agagcaacgttgcgcagtgtagtaacagtgtagcacttgct 1220
DB 10498 GCGCTTTACCCGACGATGCGAATAATCATTCATGATGATTAACCGACGACATCGGC 10439
QY 1221 cgaagctacacagtgtagaagctgtagcagctgtagcagctgtagcagctgtagcagctgtagc 1280
DB 10438 GCTCAACAGCAAGTGTGATATGCGACGTGCGGATATCAAGTCACTCTGCGCTGCAATTG 10379
QY 1281 tgcgctcaatgtagaagaaacagactgctctctctgtagcagtgtagcaggaacac 1340

DB 10378 CTTCCTATTGCTGGAGAAAAGCCGATCGCAAGTTCTGTGATTAAGCGCTGAAGATTAC 10319
QY 1341 gtagcgaatgtagcgtgtagtagaagctacacataacgtcggaagcagtgct 1400
DB 10318 CGGACACCCCGCAAGGCGTGGACGATTATGCTTAACCGACG-----AGAAAGCC 10268
QY 1401 attcaaccatgaatcgttgcctcatttgaacgagcttgtaggaatgaagtgtagtct 1460
DB 10267 ATTACCCCGCAATATGCGCGACGCAAAATTAGCATTTTCCCGCGCATGACGATTTTTC 10208
QY 1461 actgtgataccggaatgtagatgtagcagtgtagcagtgtagcagtgtagcagtgtagc 1520
DB 10207 ACCTGTGACGTTGTATGCGCAACGCTGCGCGCATGATCTC---AAATATCAAGCGC 10151
QY 1521 aagcgagcttgtagtcttcccgacagcagtgtagcagtgtagcagtgtagcagtgtagc 1580
DB 10150 AAGCGTCCCTGTTAGTTCGTTTAAACAGGTTTCATGCTTAAGCGCATGCCAGACGC 10091
QY 1581 attgtgtagcagtgtagcagtgtagcagtgtagcagtgtagcagtgtagcagtgtagc 1640
DB 10090 CTGGGTGCGACGCGACAGACAGCAAGCGTACAGTGTGCGCATGTCGCGGATGCGCGT 10031
QY 1641 ttagcagtgctgctgtagtgtagccttgtagcagtgtagcagtgtagcagtgtagc 1700
DB 10030 TTATGCAATGTGATGCGCATTTCTCTCTCAGTGTGCAATGAATACTGCAAGTGAAT 9971
QY 1701 gtagtgtagcagtgtagcagtgtagcagtgtagcagtgtagcagtgtagcagtgtagc 1760
DB 9970 GTGCTCTTTAACACAGCGTGTGCGCTTGTGCGCATGAGATGAAGCTGTGCGCTAT 9911
QY 1761 cgaagatgtagcagtgtagcagtgtagcagtgtagcagtgtagcagtgtagcagtgtagc 1820
DB 9910 TTGACTGACGCGACCGCAACAGCAAGCAAACTTTCGCGCATGTCGCGGATGCGCGC 9851
QY 1821 atcaaatcgtgtagcagtgtagcagtgtagcagtgtagcagtgtagcagtgtagcagtg 1880
DB 9850 ATTACGCGTATCCGTGTAAGAAAGCGCTGTAAGTGTATGAAGCGCTGCAACGCGCTTC 9791
QY 1881 gcatatcctgagctgtagcagtgtagcagtgtagcagtgtagcagtgtagcagtgtagc 1940
DB 9790 TCCATGACGCGTCCGCTGTTGTTGATGTGTGCTGCTGCGCAAGAGCTTATGCTATGCA 9731
QY 1941 ccaacatcagctgtagcagtgtagcagtgtagcagtgtagcagtgtagcagtgtagcagtg 2000
DB 9730 CCCGATCAAACTGCAAGCGCAAGGTTTGAAGCTGTATATGCTGCGGATCATC 9671
QY 2001 gtaggagtagtagcagtgtagcagtgtagcagtgtagcagtgtagcagtgtagcagtg 2042
DB 9670 AGCGGACGCGTATGATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 9629

RESULT 4
D90724/c 19978 bp DNA BCT 07-FEB-1999
LOCUS
DEFINITION
Escherichia coli genomic DNA. (19.4 - 19.8 min).
ACCESSION
D90724.1 GI:1651391
VERSION
D90724.1 GI:1651391
KEYWORDS
Complete and shotgun sequencing; polt; artj; arch; artc; artl;
artp; ampd; poxb; agp.
SOURCE
Escherichia coli (strain:K12) DNA, clone:Kohara clone #211.
ORGANISM
Escherichia coli
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.

REFERENCE
AUTHORS
TITLE
JOURNAL
Mori, H.
Direct Submision
Submitted (18-MAY-1996) to the DDBJ/EMBL/Genbank databases.
Hirokawa Mori, NARA Institute of Science and Technology, Res. &
Edu. Center for Genetic Info., 8916-5 Takayama, Iкома, Nara 630-01,
Japan (E-mail:hmori@itc.istc.nara.ac.jp, Tel:81-7437-2-5660,
Fax:81-7437-2-5669)
2 (sites)
REFERENCE
AUTHORS
Alba, H., Baba, T., Fujita, K., Hayashi, K., Honjo, A., Horiuchi, T.,

Ikemoto, K., Inada, T., Isono, K., Isono, S., Itoh, T., Kanai, K., Kasai, H., Kashimoto, K., Kim, S., Kimura, S., Kitagawa, M., Kitakawa, M., Makino, K., Masuda, S., Miki, T., Mizobuchi, K., Mori, H., Motomura, K., Nakamura, Y., Nishimoto, Y., Nishio, Y., Oshima, T., Saito, N., Sempel, G., Seki, Y., Tagami, H., Takemoto, K., Wada, C., Yamamoto, Y. and Yano, M.

The systematic sequencing of the *Escherichia coli* genome in Japan Unpublished (1996)

3 (sites)

Oshima, T., Alba, H., Baba, T., Fujita, K., Hayashi, K., Honjo, A., Ikemoto, K., Inada, T., Itoh, T., Kajihara, M., Kanai, K., Kashimoto, K., Kimura, S., Kitagawa, M., Makino, K., Masuda, S., Miki, T., Mizobuchi, K., Mori, H., Motomura, K., Nakamura, Y., Nishimoto, H., Nishio, Y., Saito, N., Sempel, G., Seki, Y., Tagami, H., Takemoto, K., Wada, C., Yamamoto, Y., Yano, M. and Horiiuchi, T.

A 718-kb DNA sequence of the *Escherichia coli* K-12 genome corresponding to the 12.7-28.0 min region on the linkage map DNA Res. 3 (3), 137-155 (1996)

97061202

Collaboration Information:

Project:

The Japan E. coli genome DNA sequencing project

Group:

The Japan E. coli genome DNA sequencing group

Members: (1995.4 - 1996.3)

Alba, H., Baba, T., Fujita, K., Hayashi, K., Honjo, A., Horiiuchi, T., Ikemoto, K., Inada, T., Isono, K., Isono, S., Itoh, T., Kanai, K., Kasai, H., Kashimoto, K., Kim, S., Kimura, S., Kitagawa, M., Kitakawa, M., Makino, K., Masuda, S., Miki, T., Mizobuchi, K., Mori, H., Motomura, K., Nakamura, Y., Nishimoto, H., Nishio, Y., Oshima, T., Saito, N., Sempel, G., Seki, Y., Tagami, H., Takemoto, K., Wada, C., Yamamoto, Y. and Yano, M.

Headed by:

Name: Takashi Horiiuchi

Address: National Institute of Basic Biology, Okazaki, 444, Japan

E-mail: kishori@nibb.ac.jp

Information operator:

Name: Hirotada Mori

Address: NARA Institute of Science and Technology, Ikoma, 630-01, Japan

E-mail: hmori@gtc.aist-nara.ac.jp

URL:

The Japan E. coli genome database

http://sw3.aist-nara.ac.jp

FEATURES

source

1. 19978

/organism="Escherichia coli"

/strain="K12"

/db_xref="taxon:562"

/clone="Kohara clone #211"

/map="19.4-19.8 min"

/note="Nucleotide position 898269-918246 from the initiation site of *thra* (0 min.). This clone is from Kohara lambda miniset library."

1. 208

/gene="potI"

<1. 208

/gene="potI"

/note="ORF_ID:0210#15; similar to PIR Accession Number D45313"

CDS

/codon_start=2

/transl_table=1

/product="Putrescine transport protein PotI."

/protein_id="BAA35571.1"

/db_xref="GI:1651392"

/translation="MASFVGSGATTPMLVFSSVRGKVPETNALTLGLGAVIGS FIAWYLAARAEKQIRIDIQARRG"

268. 756

/note="ORF_ID:0211#1"

/codon_start=1

/transl_table=1

/protein_id="BAA35572.1"

gene

CDS

/db_xref="GI:4062443"

/translation="MEDTEGFEKTTSSHARLVNPAVLAALATIMRGDLVMEF NTLVAGEFIHSVOTMSTLTFISIVYFELMCAPSVGRMARLYLTLOT TAAVLAASAGIGYPELFSIPGSKREIFHSLMOKLPDMLIMLFLVSTSRFFO LQ"

797. 1924

/note="ORF_ID:0211#2; similar to PIR Accession Number B64017"

/codon_start=1

/transl_table=1

/product="Hypothetical RNA methyltransferase H10958 (EC 2.1.1.-)"

/protein_id="BAA35573.1"

/db_xref="GI:4062444"

/translation="MCCATVDAGRCRSCQIMQPIPOLSAKTADLKNLADPVEEM CAPVSGEGCGRNKAARVSSVSKPILGMHNRGTEDLDCDPLPASFAVPAALK PFIARAGLTPIYNVARKRGELKYLILTSQSDGMMLFVLRSDRLAQLKALPMHE QLPOLKIVYNIQPVHMAIMGEFEIYLTGQALAEFNVPLMIRPQSFQTPVAVA SOLYATARDWVROLPKHMDLFCGVGFGIHCATPPMOLGIEIASEAIAACASOA ELGLRLOFOLDSTOFATQGDVPELVNPPRGIGKPLCDYLSTMAPRFIIYSSC NAOTMARDIRELPFRIERQDLPMPFHTAHYEVLTLLVQO"

complement(2123. 2854)

/gene="artJ"

complement(2123. 2854)

/gene="artJ"

/note="ORF_ID:0211#3; similar to PIR Accession Number I40995"

/codon_start=1

/transl_table=1

/product="Arginine-binding protein ArtJ."

/protein_id="BAA35574.1"

/db_xref="GI:1651393"

/translation="MKRLVLAALASFTFGSAAEKINFGSATYPPESIGNNEIV GFQIDLAKLCKQWQACFTNNHAFDLSISIKRKYDAVIRKDYATIPRESQSPFT PYNSAVVIAKRTYTPADLKRRIGMENGTHQRTODQPEVATVSIDTONAF IDLNGRIDVFGDTAVVNEMLKTPNPGVATEKVDVDFGGLGIAVPDKKALLE KLNNAIAIKADGYOKISDQWEPQ"

complement(3145. 3813)

/gene="artM"

complement(3145. 3813)

/gene="artM"

/note="ORF_ID:0211#4; similar to PIR Accession Number S31730"

/codon_start=1

/transl_table=1

/product="Arginine transport system protein ArtM."

/protein_id="BAA35575.1"

/db_xref="GI:1651394"

/translation="MEFYLPKLGHTSLTVASLIALILALFTITLTKTPVL VMUVRGYITLFTGTPILVQIFLIYGGQPTIQEYPAHLSEPMICALILSINS AAYTOLFYCAIRAIPEGWOSGALGMSKDTLAILPYAPFRISYSSENVIVKX STSLAVYITLMEVWGSQLLXGRITVDVNGVAGAGIITLVVNGLITLMRLIEKALAF ERRN"

complement(3813. 4529)

/gene="artQ"

complement(3813. 4529)

/gene="artQ"

/note="ORF_ID:0211#5; similar to PIR Accession Number I40993"

/codon_start=1

/transl_table=1

/product="Arginine transport system protein ArtQ."

/protein_id="BAA35576.1"

/db_xref="GI:1651395"

/translation="MNEFPPLASAGWVGLACALIVGIALMFPAWESAKWRVA WASSALVITIRGPELIVYFITGSSQLLITLSDGTTNLGFGVQIPVDQLENDVVS FPLCGVTAUSLTYAAYASQTLRKALAVPGWESQALGSAIFRFLVMOQMRH ALPGLGQWLVLLKDALVSLISVNDLMOTKSIARTQEPFTWYVAAAIYLVITLL SOYTIKRIDLRATFRFRS"

complement(44536. 5267)

/gene="artI"

complement(44536. 5267)

/gene="artI"

/note="ORF_ID:0211#6; similar to PIR Accession Number S54109"
/codon_start=1
/transl_table=11
/product="Arginine binding protein art1"
/protein_id="BAA35577.1"
/db_xref="GI:1651396"
/translation="MKVLIALIAGFSLSAETAETIRPEATSEYPPESIDANNOIV
GEVDLQALKEIDATCFESNOAFSLPSEKFRVEAVMAGMDITPEREKVLETT
PYSDALFVGQGGKTSYDOLKGGKVGQNGTTHQKFTMDKHPEITTYPYDSYONAK
LDLONGRIDGVGDAVYVTEMLKDNPKLAAGDKVTDKDYFGIGLAIARQGTLELO
KLNTALEKKKQGTETTYTNKMFQK"
/complement(5285..6013)
/gene="artp"
/complement(5285..6013)
/note="ORF_ID:0211#7; similar to PIR Accession Number S31694"
/codon_start=1
/transl_table=11
/product="Periplasmic transport system protein Artp."
/protein_id="BAA35578.1"
/db_xref="GI:1651397"
/translation="MSIQNGINCFYGAHQALFDITLDCPQGETLVLLSPGAGKSL
LRLVNLLEMPRSGTLMIAQNHFDFTPTSPDKAIRDLRNMGVFOQYNIPLHLYOON
LLEAPCRVLGSKDQALARAELERLRKPYSDRPLHLVSGQOORVALARALMEP
OYLEDEPTALADPEITTAQIVSIIRLAEITNITQIVTIVEVEARKTASRVYMEGH
IYEGDASCFTEPQEPKYNLYSH"
/complement(6231..6746)
/note="ORF_ID:0211#8"
/codon_start=1
/transl_table=11
/protein_id="BAA35579.1"
/db_xref="GI:4062445"

Query Match 14.1%; Score 305.2; DB 2; Length 19978;
Best Local Similarity 50.7%; Pred. No. 2.9e-70;
Matches 873; Conservative 0; Mismatches 828; Indels 21; Gaps 5;

QY 327 atggcacaacgagcgaagacaatlaattgacaccltggaaagtcgaagtcgtgaagcga 386
DB 13328 ATGAAACAAACGGTTCACGCTTATATCGCCAAAACACTCGAATCGGCGGTAACCGC 13369
QY 387 attatcgtgttggctggcgaagccttaa---tcggaatcgtgaatgctgcgcgaatca 443
DB 13268 ATCTGGGAGTTCACAGCGGCTCTGCAACGGCTTAGTACAGTCTTAAATCGCATGGCC 13209
QY 444 gatattgagtggtgacgcttcgaatgagaagcgagcgcttctgcagcggtgcgaa 503
DB 13208 ACCATCGAGTGTATGTCACCGCCGACGAGAAGTGGCGCTTGGCGCTGGCGCTGAA 13149
QY 504 tctgtatcactcgtggagcgtgcgaatgctgtcgtctctgtgtgctcctggaacaacacac 563
DB 13148 GCAACAACCTTAGCGGACAACTGCGGCTCTGCGCGGATCTGCGCGCCCGCAACCTTGAC 13089
QY 564 ctgattcgaaggtcttattgattcgcacatcgaaatcggtgcgaagtggttggcactgcagc 623
DB 13088 TTAAATCAGCGGCTGTTGATGTCACCGCAATCAGCTTCCGGTACTGGGATTTGCCGCT 13029
QY 624 catattcgaagtgccgaagattgctcgaagcttctccagaagaacgcacatccggaatttg 683
DB 13028 CAAATTCCTTCAGCAAGAAATTTGACGAGGCTATTTCCAGAAACCCACCAAGACTA 12969
QY 684 tctaaagaatgctcgttctcgtcgaatggtgaatggtggaagcgggtgaaagcact 743
DB 12968 TTCCGCGCAATGTAGTCACTATTCGAGCTGTTCACGCGGACGAGTCCCAAGTA 12909
QY 744 tctgatacgcgaattcagtcacacatgycgggttaaaggctgttcggtgagtgatctcc 803
DB 12908 CTGGCGATTCGCAATGCGCAAGGCGTCTTAACCGTGGCTTTGCGTTCGTTGTTACCA 12849
QY 804 ggtgatacgcgaatgagaagcgaagtgacgtaactatcctaattcactatcttct 863

DB 12848 GCGCAGCTGGCGTTAAACCTGCGCCAGAAAGGCGC---AACATGACATGCTATCATCGC 12792
QY 864 gcaatcctgtgtgtcccggaatcctactgaaggctcgaagcgtggtgagcgattaac 923
DB 12791 CCACACCACTGCTGACGCGCGGAGAAAGATGATACCAAACTGGCGCACTCTCGCT 12732
QY 924 aacgtatgctcgtcacttctgtctcgtcgtgctggaagaaatgctcgcgcgaagt 983
DB 12731 TATTCAGCAATATGCGCCCTGATGTGTGGACGCGGTGCGGGGGCGCAATAAGAGTTA 12672
QY 984 ttagagcttgcggaagaatataacacgaatcgggaatcgcgtggtggtlaagcaat 1043
DB 12671 GTTACGATTCGCGGAAATTTAAAGCCGCTATGTTGATGCTGCCGCGGTAAGAACAT 12612
QY 1044 atcgaatgagaatcgcgttgaagtggaatggaatggaatggaatggaatggaatgga 1103
DB 12611 GTGCAATACGATATCCGTTATGATTTGGAATGACCGGTTAATGCGCTTCTCTCAGGT 12552
QY 1104 gtgagtgctccaaatgagcgaatcgtcgtatcactatggtlaagcgaatcctatct 1163
DB 12551 TTCCATACCATGATGAAAGCGCGACGCTTAGTGTACTCGGCAAGCAATTCCTACCGC 12492
QY 1164 gattccttcccta---aagacaacgttgcgaagtggaatcgaatcgaatcgaatcga 1220
DB 12491 GCTTCTACCCGACCGCATGCGCAAAATCATTCAGATTGATATCAACCGACGATCGGC 12432
QY 1221 cgaagtcacagcggtgaagatcgcgtggaacggtgagtggtctgtaacaatcgaataat 1280
DB 12431 GCTACAGCAAGGTGATATGCGCATGTGCGCGCATATCAAGTCACTCTGCGCATTTG 12372
QY 1281 ttcgctcatgltgaagaaacacagatcgttctccttctgacgtcgaatcgaagcgaac 1340
DB 12371 CTTCATTTGGTGGGAAAGAAAGCCGATCGCAAGTTTGTGATTAAGCGCTGGAAGATTAC 12312
QY 1341 gaagcgaatgagtcgtgtgtagaagacgacacataacgltcgaagaacgtgct 1400
DB 12311 CGCGACCGCCGCAAGGCGTGGACGATTTAGCTAAACCGACCG-----ACAAAGCC 12261
QY 1401 attacacctgaatcgttgcctcctatcttgaagacgcttgcggaatgaagatgagtgct 1460
DB 12260 ATTCACCCGCAATTCGCGCGCACCAATTAATGATTTTGGCGCGATGACGCTATTTTC 12201
QY 1461 acgtgataccgacgtcgtcaatgtgtgcaatgacgtgacgtgacgtgacgtgacgtgac 1520
DB 12200 ACCGTGACGTTGTTAGCGCAACGCTGTGGCGGACGCTTCTT---AAAATATACGCG 12144
QY 1521 acgcgcaacttgtggttcaatcgcgaacgacgacgtgacgtgacgtgacgtgacgtgac 1580
DB 12143 AAGCGTGGCTGTTAGGTTGTTAAACCGCGTTGATGGCTAACGCGCATGCGCGACGCG 12084
QY 1581 attgtgtcgaagaatgltgtatcgaacacgacgacgtgacgtgacgtgacgtgacgtgac 1640
DB 12083 CTGGTGCAGAGCGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 12024
QY 1641 ttgggcaatcgtcgtgtggttgccttgcacgttgaagctgcacacacacacacacacacac 1700
DB 12023 TTTAGCATGTTGATGAGGCGATTTCTCTCACTAGTACGATGAATACCTGCAATTAAT 11864
QY 1701 gtgtgtttaaacaacgttcttctggaatggtgaatggaatggaatggaatggaatgga 1760
DB 11963 GTGCTCTTTAAACACACGCTGCGCTGCGCTTGTGCGATGGAATGAAGCTGCGGCTAT 11904
QY 1761 ccgaatctgttctcgtcgaatggaatggaatggaatggaatggaatggaatggaatgga 1820
DB 11903 TTGACTAGCGGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 11844
QY 1821 atcaaatcgttgcac 1880
DB 11843 ATTAGCGGATTCGCTGTAAGAAAGCGCTGTAAGATGTAAGCTGTAAGCTGTAAGCTGTA 11784
QY 1881 gcatatcctggaacgttgcac 1940
DB 11783 TTCAATGACGCTGCGCTGTTGTTGATGATGATGATGATGATGATGATGATGATGATGAT 11724

Qy 1941 ccaacacatcagtggaacaggtlcatlgaaggaagcgccacccgaacgctt 2000
11 1111 111111 11 111111 11 1111 11 1111
Db 11723 CCGACATCAAACTCGAACAGCGCAAGGTTTCAGCCTGTATATGCTGGCGGAATCANC 11664
Qy 2001 ggttgagagagtgagagcgatgatcgatcgcccgcttgcgaac 2042
11 1111 111111 111111 1111 1111
Db 11663 ACGGACGCGGTGATGATGATCGAATCGCGCAAAACAAAC 11622

RESULT 5
ECOPORX 1719 bp DNA BCT 05-OCT-1995
DEFINITION Escherichia coli pyruvate oxidase (poxB) gene, complete cds.
ACCESSION M28208 J04957 M11712
VERSION M28208.1 GI:1009024
KEYWORDS alpha-peptide; flavoprotein dehydrogenase; poxB gene; pyruvate oxidase.
SOURCE Escherichia coli (strain K-12) DNA.
ORGANISM Escherichia coli
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia.
REFERENCE 1 (bases 1 to 1719)
AUTHORS Grabau C., Chang Y.Y. and Cronan J.E. Jr.
TITLE Lipid binding by Escherichia coli pyruvate oxidase is disrupted by small alterations of the carboxyl-terminal region
JOURNAL J. Biol. Chem. 264 (21), 12510-12519 (1989)
MEDLINE 89308683
COMMENT On Oct 6, 1995 this sequence version replaced gi:341661.
FEATURES
Source location/Qualifiers
1..1719
/organism="Escherichia coli"
/strain="K-12"
/db_xref="taxon:562"
1..1719
/gene="poxB"
1..1719
/gene="poxB"
/codon_start=1
/transl_table=1
/product="pyruvate oxidase"
/protein_id="AAB59101.1"
/db_xref="GI:1009025"
/translation="MKQTVAVYIAKLTESACVKRWVGTGDSLNGSLSDSLNRMGTIEN
MSTRHEEVAAPAGAEALQSLGELAVCAAGSCGPNLHLNGLFDCRHNVPLVLAIAHL
PSEISGSEYFQETHPOELFRECHSHYCELVSPEDIPQVLAIAKRAVLRVSVVLP
GVDAIKAPBEGATMHWYHAPQVPTPEEELRLKLAOLIRSSNTAIAIMGSCAGAHKE
LVERAGIKAPIVAHLRGKEHVEDNPDMTCGLIGSSSFTHMNAADTVLIGTGF
PYRPFYPTDAKIIIDINPASTGAHAKYDALVGDINSTLALPLVEEKDRFLDK
ALEDYRDARKGLDLAPSEKAHHPVLAIEHSHPAADALFTDVGTPVMAARYLK
MNGKRLIGSFNHSNMANAPHGVAQATEPEROVVAMCGDGSMTMGDELVSVMYK
LPVKLVFNNSVLTGFVAMENKAGVLTNDGTEHLDTNPAIEACGIGIRVEKASEVD
EALQRAFSIDGPVLVDVVAKEELAIIPQIKLEQAKGSLIYMLAIIISGRDEVIELA
KTNMLR"
1597
variation /gene="poxB"
/note="mutant poxB11"
/replace="a"
1647
variation /gene="poxB"
/note="mutant poxB6"
/replace="a"
1658
variation /gene="poxB"
/note="mutant poxB14"
/replace="t"
1678. 1679
variation /gene="poxB"
/note="mutant poxB15"
/replace="cc"
1690. 1691
variation /gene="poxB"
/note="mutant poxB7"

variation /replace="t"
1690. 1691
/gene="poxB"
/note="mutant poxB16"
variation /replace="cc"
1710
/gene="poxB"
/note="mutant poxB8"
variation /replace="a"
1714
/gene="poxB"
/note="mutant poxB10"
/replace="g"
BASE COUNT 418 a 446 c 483 g 372 t
ORIGIN

Query Match 14.0%; Score 302; DB 2; Length 1719;
Best Local Similarity 50.6%; Pred. No. 2,1e-69;
Matches 871; Conservative 0; Mismatches 830; Indels 21; Gaps 5;

Qy 327 atggcacacagcttaagcagaacaattatgacacttgggaagctcaagtggtgaagga 386
11 1111 111111 111111 1111 1111 1111 1111 1111 1111
Db 1 ATGAACAAACGCGTTGACGCTTATATCCGCCAANAACATCGAATCGCGAGGCGTGAACGC 60
Qy 387 attatggttggttggtgacagccttaa---tccgatcgtgatgctgtccgcaatca 443
11
Db 61 ATCTGGGAGCTCACAGCGGACCTCTGAACGCTCTTAGAGACAGCTTATATCGCATGGGC 120
Qy 444 gatattgagtggtgacagttcgaaatgaagaagcggcggtttgcaagcggtgagga 503
11 111111 11 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
Db 121 ACCATCGAGTGATGTCCACCGCCGCAAGAGAGGCGGCTTGGCGCTGGCGCTGAC 180
Qy 504 tctgtgacacagtggaagctggaatgatgtgtcttcttctgtgtgtcctggaaacacac 563
11
Db 181 GCACACTTACGCGAAGACTGGCGGTCTGCGCGGATCGTGGCGCCGCAACCTGAC 240
Qy 564 ctgattcagggtcttattgatctgcatacgaaatggtgcaaggtgttgccatcgtagc 623
11
Db 241 TTAATCAACGGCGCTTGTGATTCGACCGCAATACAGTTCGCGTACTGCGCATTCGCCCT 300
Qy 624 catattcggagtgccagattggttcgaagcttcttcagaagaacgacatccgagatttg 683
111111 11 1111 11 1111 1111 1111 1111 1111 1111 1111 1111
Db 301 CATATTCCCTCCAGCGAATGGCAGCGCTATTTCACAGAAACCCACCAAGAGCTA 360
Qy 684 ttaagaagatgctcgtgattcagcagaatggtgaatggtgtgtgtgagcaggtgaacgact 743
11 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
Db 361 TTCCCGAATGATGACTATTGCGAGCTGTTTCCACCCCGAGACAGATCCCAAGTA 420
Qy 744 ttgcatacgcgattcagtcacacatgycggtlaaagggtgtcgtgtgtagtattcct 803
11
Db 421 CTGGCGATTGCCATCGCAAGCGGCTGTTAACCGTGGCGTTCGCTGTGCTTACCA 480
Qy 804 ggtgatcgcgttaagaagcaggtgaagcttacttcccaattccataattctct 863
11
Db 481 GCGCGAGTGGGCTTAAACCTCGCGCCAGAGAGGGGC---AACCATGCACTGTATCATTCG 537
Qy 864 ggcactcgtgtgttcccgatcctactgaagctgaagcgtgtgtgtgaagcgattaac 923
11 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
Db 538 CCACACCAAGTCGTGACCGCGGAGAGAGAGTTAGCCAAACTGCGCAACTGCTGCGT 597
Qy 924 aagcctaagcttgcacttcttctgcgtgcygagcgtgaagaatgctgcgcgcaggtg 983
11
Db 598 TATTCACACCAATATCGCCCTGATGTGTGCGACGCGCTCGGGGGGCCCAATAAGAGTTA 657
Qy 984 ttgaggttgcgcggaagaatcaatcacagatcgaggcaatgcgttgggtgaagcagtlac 1043
111111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
Db 658 GTTGAGTTGGCGGGAATTAAGCGCCTATTGTTCAATGCCCTGCGCGGCAAGAACAT 717
Qy 1044 atccagcagtaagcagcttgaagtggtgcagatgctgtgcctgtgttaagcgccctgc 1103
11
Db 718 GTCCGATACGATATTCGATGATGTTGGAATGACGGGCTTAATCGGCTTCGTCAGAGT 777

Oy	1104	gtagagcguccaaatgaggagatctgcgagatctatcttggtgaagatctccatattc	1153
Db	778	TTTCATACATGATGAACGCCGACAGCTTAACTGCTACTGCGACCGAATTTCCCTACCCG	837
Oy	1164	gattctccctccta---aaagaaacgtctgcacagtgagatatacaacagctgcacatlgct	1220
Db	838	GCCTTACCCGAGACCGATGCGCAAAATCATTTAGATTGATATCAACCGACGATCGGC	897
Oy	1221	cgacgtaccagctggaagtatccggtgacccggtgatgtctgcgcacaacatcgaaaaatac	1280
Db	898	GCTCAGACGACGATGCGATATGGACATGTCGCGGATATCAAGTCACATCTGCTGCATTTG	957
Oy	1281	ctgcctcagctggaagggaaaaaacaagatctctctccctctgacgagatctaaagcaaac	1340
Db	958	CTTTCATTTGGTGGAAGAAAAACCCGATCCGACATTTCTGGATTAAGCCGTGACACATTAC	1017
Oy	1341	gagcgtaaagtgcgtcctgcgtgtagagacgtacacacataacgcttcgaaagacatlgctc	1400
Db	1018	CGCAGACCGCGCAAMAGGGCTGGAGATTTTAGCTAAMACGAGG-----AGAAACCC	1068
Oy	1401	attacccctgaaatacgtctgcctctatcttgaacagcgtgcgcagataagatgctgctt	1460
Db	1069	ATTTCACCCGCAATATCTGCGCGCACAGAAATTTAGCATTTTGGCCGATACAGCTATTTC	1128
Oy	1461	acgtggaataccgacatgagcaatggtgagcaatgagagatacatcgaaatcccgaaagga	1520
Db	1129	ACCTGTGACCTTGGTACGCCAACGGGTGGCGCGCACGTTATCT---AAAATGAACGC	1185
Oy	1521	acgcgcacatctggtggtctcaatccgcacagcagatgctcaatgctctgcctcaatcgc	1580
Db	1186	AAGGTCGCCCTGTTAGTTTGTGTTTAAACAGCGTTGATGGCTAAGCCATGCGCAGCGC	1245
Oy	1581	atggtgcgcaaaagtgtgtgaatcgaaacccgacagtgatcgcgtgtgtgcgtgagtggt	1640
Db	1246	GTCGGTCCGACGACGCGACAGCGCAAGACGTCAGGTGTCGCATGTGCGCGATGGCGGT	1305
Oy	1641	ctggagatcgtcgtcgtgggtgagctcttcgaacggttaagctctgacaaatctccgctgaagct	1700
Db	1306	TTTAAAGCATGTTGATGGGCGAATTTCTCTAGTAGTCCATGATCAATCAATCCAGTGAATTT	1365
Oy	1701	gtggtgtcttaacaacaagatctctctgggacatcgtgtgaagtctggaatgctcgttggaaggaac	1760
Db	1366	GTCGCTTTTAAACAGCGCGTGGGCTTTGGGGGATGGAGATGAAGAATTAAGCTGGGCTAT	1425
Oy	1761	ccgaattctgttactgcacatgaagaaagtgaattccgacagaaattgcgcgcgtgcgtgtc	1820
Db	1426	TTTGACTCAGCGCACCGCAATACACGACACAACATTTGGCCGATTGGCCGAAGCGTGGCGC	1485
Oy	1821	atcaaatctgtaacgcatacaacccgataccgaagaagatctcggagacagctgcgcgaagatlg	1880
Db	1486	ATTTCGCGGTATCCCTGTAGAAAAGAGCTCTGAAAGTTGATGAAGCCCTTCACACCGCCCTTC	1545
Oy	1881	gcaatactctggaacctgtactgatactgatactcgtcaacagatccataatctgctctgcataccca	1940
Db	1546	TCCATCGACGCGTCCGGTGGTGGATGGGATGGGATGGGATGCCAAGAAGATTAAGCATTTCA	1605
Oy	1941	ccaacacatcaagtgtggaacagatcatalgtggaattccgaagaagcgcacaccggaacgctctt	2000
Db	1606	CCGCGATCAACATCCCAACAGCCCAAGCTTTACGCGCTTATATCTTACCGCATCATCTC	1665
Oy	2001	ggtggagagatgaagacgagatcgaatctggcccgctcgaac	2042
Db	1666	AGCGGACCGCGTATGAAGTATCTGAAGTATCGGCAAAACAAAC	1707

RESULT	6
ECOPONB10G	
LOCUS	ECOPONB10G 1719 bp DNA BCT 05-OCT-1995
DEFINITION	<i>Escherichia coli</i> (mutant posx10) pyruvate oxidase (posx) gene, complete cds.
ACCESSION	L47688
VERSION	L47688.1 GI:1009026
KEYWORDS	alpha-peptide; flavoprotein dehydrogenase; posx gene; pyruvate

SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	FEATURES
source	oxidase. Escherichia coli (individual isolate mutant poxB10, strain K-12)	1 (bases 1 to 1719)	Grabau, C., Chang, Y. Y. and Cronan, J. E. Jr.	Lipid binding by Escherichia coli pyruvate oxidase is disrupted by small alterations of the carboxyl-terminal region	J. Biol. Chem. 264 (21), 12510-12519 (1989)	89308683	Location/Qualifiers I. 1719

gene	1. .1719
	/gene="poxB"
CDS	1. .1719

```

/note="mutant poxB10: Arg-572 --> Gly; A -->G at 1714
/codon_start=1
/transl_table=11
/product="pyruvate oxidase"
/protein_id="AAB59102.1"
/db_xref="ec:1.000003"

```

variation

translation="MKTQVAAVYIAKTTLESACVKTWGTGSLNGDSLRMOTTIEM
MSTRIEEVAAGAEALSGELAVCAGSCGPNGLHINGLFGDCHNRHNPVPLATIAHII
PSDGLSPGTPOTHPOELLFRECISHYCELVSPEDTIOPLATAMKAVLNGSCVYVLP
GVATLAKPPEGATMHNITAPROPVYTPEEELRKLQOLIRYTSNIALMAGTSCSACANHE
LVERGKTIKAPLVALHNGKEHVEYDNPDPVCMGTGLIGSSCFSTHMANADTLYVLGTGPF
PIYRAYPDAKATLIDINPDSKISAGHSDALVSDITSTLALLPIVEBKNDARFLDK
ALIEDYDARKGIDDLIDPSEKAIHPQVYLAHESHPADDAITCDVCTP'YVWARYVLT
NMGRKVRNNSYHSGSNAMAPHGVAQNTDEEPROYVAVACGGSGTLMGDELIVOKMK
LPVCLFVFNNSYSLGVANEMKAGGLDTGTLHTPNFARIEACGTSITRPERKSPVD
EALQAFESIDGEPVLVDVYVAKBELAIIPQITLBDQAGFSLMLNAIISGRDEVIELA
KTNMLG"

1714

```

/notes="mutant posB10: Arg-572 --> Gly"
/replace="a"
BASE COUNT      417 a      446 c      484 g      372 t
ORIGIN

```

Query Match	14.0%;	Score 302;	DB 2;	Length 1719;
Best Local Similarity	50.6%;	Pred. No. 2.1e-69;		
Matches 871;	Conservative 0;	Mismatches 830;	Indels 21;	Gaps 5

QY 327 atggcaccagcctcagcaggaacaattatgacaccttggaaagctcaaggtgttaagcga 388
 Db 1 ATGAACAACAAACGGTTTGGACGCTTATATGCCCAAAACACTCGATAGGGCGGGGTAAACGC 60
 QY 387 attataggcttcggttgcggttgacagcccttaa---tcgcagtcgtgagtcgtcgcgaatca 44
 Db 61 ATCTGGGGAGTCCACAGGGGACCTCTCTGAAACGCTTCTAGTACACTTTAAATCGCATGGCC 120
 QY 444 gattttgagtggtgtgcacgcttcgaatgaagaaagcggcgcttttgaacccggttgcgaa 503
 Db 121 ACCATCGAGTGGATGGCTCACCCGCCAGAGAAAGATGGGGGCTTTGGCGCTGCGCGTGA 180
 QY 504 tctgtgtaactctggggagcttgagcagttgtgtctctctgtgttctctgaaacaacacac 56
 Db 181 GCACAACCTTACCGGAAGAACTGGCGGTGTGCCCGGAGTCTGTCGGCCCCCGCAACCTTCAC 240
 QY 564 ctgattcagagtcctcttctgattcgcattcgaacaaatgtgcgaagtggttggccatcgtcagc 623
 Db 241 TTATTAACAGGGCCGTGTTCGATGGCCACCGCAATCAGCTTCGCGTACTGCGGATTCGCCGT 300
 QY 624 catattccagagtcgccagatgtgttcgacgcttcttccagaagaacgcataccggagatttgg 683

Db 301 CATATTCCTCCAGAGGAATTTGGAGCGGCTATTTCAGAGAAACCCACCAAGAGCTA 360
 Oy 684 tttaagaaatcctctgttactgtgagatggtatgtgtgtgtgagcaaggtgaagcatt 743
 Db 361 TTCCGCGCAATGTAGTACATATTTGCGAGCTGTTTCCAGCCCGGAGCAATCCCAAGTA 420
 Oy 744 ttgcatcagcattcagccac 803
 Db 421 CTGCGGATTTGGCATTGCGCAAAACCGTCTTAACCTGGCGCTTTGCGGTGTCTGTACCA 480
 Oy 804 ggtatcatcgtctaaagaaagcaaggtgacgttactatcccaattccatttctct 863
 Db 481 GCGCAGCGGTGTTAAACCTGCGCCAGAGAGGGGCG---AACCATCATGTATCATGCG 537
 Oy 864 ggcactcctgtgtgtgtcccgatcctactgagctgcaagcgtgtgtgtgtgtgtgttac 923
 Db 538 CCACACACAGTGTGACCGCCGAGAGAGAGATTACGCAAACTGCGCAACTGTCGCT 597
 Oy 924 aacgttaagctgtcacttctgtcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 983
 Db 598 TATTCACACATATTCGCGCTGATGTGTGCGAGCGGCTGCGCGGCGCGCATTAAGATT 657
 Oy 984 ttggaattgtgagaaagaaatcaatcacacacacacacacacacacacacacacacac 1043
 Db 658 GTTGAGTTTGGCGGGAATTAACGCGCTATTGTTCATGCGCTGCGGTAAAGACAT 717
 Oy 1044 atccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1103
 Db 718 GTTCGATATCGATATTCCTATGATGTGTGATGACCGGTTATGCGCTTTCGTCAGGT 777
 Oy 1104 gtgagctgtcacaatgagagcagcagcagcagcagcagcagcagcagcagcagcagcag 1163
 Db 778 TTCCATACCATGATGACCGCGACACGTTAGTGTACGCGACCAATTCCTACCGC 837
 Oy 1164 gatttccttcta---aagacaagctgtcccgatgtgatatcaaggtgtgtgtgtgtgtgt 1220
 Db 838 GCTTCTCTACCGCGAGGATTAACGCGCTATTGTTCATGATGATTAACCGCGCATCGCG 897
 Oy 1221 cgaagctacacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1280
 Db 898 GCTCAGCAGCAAGTGTGATGACGCTGTCGCGCATATCAACTCCACTTGGGTGATTTG 957
 Oy 1281 ttgcatcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1340
 Db 958 CTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1017
 Oy 1341 gagcgttaagctgt 1400
 Db 1018 CGCGACGCGCGCAAGGCGCTGACGATTTAGCTAAACGAGCG-----AGAAAGCG 1068
 Oy 1401 attcacctgaatacgt 1460
 Db 1069 ATTCAACCGCAATATCTGCGCGACGCAAAATTAATTTTGGCGCGGATGACCTTATTTTC 1128
 Oy 1461 actgt 1520
 Db 1129 ACCGTGACAGTTGTGACGCAAGCGTGTGCGCGACGCTTATCT---AAAATGAAGCGC 1185
 Oy 1521 aacgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1580
 Db 1186 AAGCGTGTGCGCTGT 1245
 Oy 1581 attgt 1640
 Db 1246 GTGGGTGCGGACGCGACAGACGCAACGCTCAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1305
 Oy 1641 ttgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1700
 Db 1306 TTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1365
 Oy 1701 gttgt 1760
 Db 1366 GTGCTTTTAAACACAGCGT 1425

Oy 1761 ccagaattgttactgtaccatgaggaagtgaatttcgcagagaattgcgcggtgtgcggt 1820
 Db 1426 TTGACTGACGGCAGCGGACTACACGACACAAACTTTGCCCGGATTTGCCGAGCGCGC 1485
 Oy 1821 atcaaatcgtgtacgacatccagcagcagcagcagcagcagcagcagcagcagcagcag 1880
 Db 1486 ATTACGGGTATCCGTGTGAAAAGAGCTGTGAAATGATGAAGCCCTCAACGCGCTTC 1545
 Oy 1881 gcatctcgtacgt 1940
 Db 1546 TCCATGACGGGCTGT 1605
 Oy 1941 ccaaccacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2000
 Db 1606 CCGCAGATCAAACTCGAACAGCGCAAGGTTTCACCTCTATATCTGCGCGCAATCATC 1665
 Oy 2001 gttgagagagtagagagcagatgacgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2042
 Db 1666 AGCGAGCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1707

RESULT 7
 ECOPOXB11G 1719 bp DNA BCT 05-OCT-1995
 LOCUS
 DEFINITION Escherichia coli (mutant poxB11) pyruvate oxidase (poxB) gene, complete cds.
 VERSION L47689.1 GI:1009028
 KEYWORDS alpha-peptide; flavoprotein dehydrogenase; poxB gene; pyruvate oxidase.
 SOURCE Escherichia coli (strain K-12) DNA.
 ORGANISM Escherichia coli.
 Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia.
 REFERENCE 1 (bases 1 to 1719)
 AUTHORS Grabau,C., Chang,Y.Y. and Cronan,J.E. Jr.
 TITLE Lipid binding by Escherichia coli pyruvate oxidase is disrupted by small alterations of the carboxyl-terminal region
 JOURNAL J. Biol. Chem. 264 (21), 12510-12519 (1989)
 MEDLINE 89308683
 FEATURES
 source Location/Qualifiers
 1..1719 /organism="Escherichia coli"
 /strain="K-12"
 /db_xref="taxon:562"
 1..1719 /gene="poxB"
 1..1719 /gene="poxB"
 /codon_start=1
 /transl_table=1
 /product="pyruvate oxidase"
 /protein_id="AAB58103.1"
 /db_xref="GI:1009028"
 /translation="MKQTVAAVIAKTTESAGVKRTWVGTGSLNGLSLDSLRMGTIEV
 MSTRIEEVAAPAAAGAEALGSELAIVCASCPGPIHLINGLFDRHNRVPLATAAHL
 PSSIEGSGYFOETHELFRCSHVELSVSPEDIPVLAIAKRAVIAIRGVSIVPL
 GDVALKPAPECATMHWYAAPOVYVPEEELIRKLAOLIRASNTAALMGSGCAGAHKE
 LVERAPKRIKAIYVARLRKEHVEVDNPDVCMGILIGSSGFHTMMAADPTVILCTOF
 PYRAVPTDAKTIQIDINPASTIGASHKVDMLVGDIKSTLALLPLEEKADRFLEK
 ALEEDYRDARKGLDLAKSEKAHHPQYLAHESHPAADDALEFCDVGTPTVAAARYLK
 MNGKRRLGSFNHNSMANAMPHGVGAQATEPEROVNAMCGDGSMLMGDPLSVOMK
 LPKIVVFNNSVLGEVAMEMKAGVLTGDTGLHPTNFAIRIAEACGITGIRVEKASEVD
 EALRAFSIDPEVLVDVVAAMEELIIPQIKLEQAKFSKSLMAHAIISGRDEVIELA
 KTNMIR"
 1597 /gene="poxB"
 /note="mutant poxB11; Ala-533 --> Thr"
 /replace="a"

variation
 BASE COUNT 419 a 446 c 482 g 372 t
 ORIGIN

Query Match 14.0%; Score 302; DB 2; Length 1719;
 Best Local Similarity 50.6%; Pred. No. 2.1e-69;
 Matches 871; Conservative 0; Mismatches 830; Indels 21; Gaps 5;

```

QY 327 atggcgcacagctagcgaaacaaatlaattgaactttggaagctcaagtgtaagcgaa 386
DB 1 atgaaacaaacggtgcttattatcgcccaaaacactcgaaatggcaggcggaacgc 60
QY 387 attatagcttggtgggagacagcctaa---tcgactcgtggaagctgctgcgcacaa 443
DB 61 atctggggagctcagcagccactcttgaaacgctttagtgaactttagtccatggcc 120
QY 444 gatattgagtggtgtgacgcttcgaaatgaagaaacgagcgagctgttcagccggtgagaa 503
DB 121 accatgagatgagatgacacccgcacgaagaaagtgccgcttgcgcgtgcgcgtgaa 180
QY 504 tegtgtgacacgtgagagctgagcagatgtgtctgtcttctgtgtgtccctggaacacac 563
DB 181 gcacaaactttagccgacacgactgctgctcccgatgctgcccgcacacacacacac 240
QY 564 ctgattcagaggtctttagtgcacacacacacacacacacacacacacacacacacac 623
DB 241 tttaattcaacgagcttgcattgctccacacacacacacacacacacacacacacac 300
QY 624 catattcagagtgagcagacacacacacacacacacacacacacacacacacacacac 683
DB 301 catatttccctcagcagaaatttgccacacacacacacacacacacacacacacacac 360
QY 684 tttaagaaatgctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 743
DB 361 ttcccgcaattgactgactgactgactgactgactgactgactgactgactgactgact 420
QY 744 tgcacacacgagcttgcacacacacacacacacacacacacacacacacacacacac 803
DB 421 ctggcagattgctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 480
QY 804 ggtgtatctgacaaagaaacgagtgagcttactatcactatcactatcactatcact 863
DB 481 ggcgagctgagcttgaataacacacacacacacacacacacacacacacacacacac 537
QY 864 ggcacacacgagcttgcacacacacacacacacacacacacacacacacacacacac 923
DB 538 ccacaaacacacacacacacacacacacacacacacacacacacacacacacacacac 597
QY 924 aacgctaaatctgtcacttctgtcacttctgtcacttctgtcacttctgtcacttct 983
DB 598 ttattccagcaattatccctctgactgtgacacacacacacacacacacacacacac 657
QY 984 tgcagctgagcagaaagaaatlaaacacacacacacacacacacacacacacacacac 1043
DB 658 gttgagattggcgggaataattaaagcctattgttcatgtccctggcggttaaaagaa 717
QY 1044 atccagcagatgaatcgttctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1103
DB 718 gtccgaattacgaataatccctgtatgtttgaatcaccgctgttattcggctgaggt 777
QY 1104 gtgagagctgacaaatgaagacacacacacacacacacacacacacacacacacac 1163
DB 778 ttccatattacatgtaaacacacacacacacacacacacacacacacacacacacac 837
QY 1164 gatttctcctccta---aagacacacacacacacacacacacacacacacacacacac 1220
DB 838 gctcttaccgacgacgacgacgacgacgacgacgacgacgacgacgacgacgacgac 897
QY 1221 ggaagcagacagtgatgaatcgcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1280
DB 898 ccttcacacacacacacacacacacacacacacacacacacacacacacacacacac 957
QY 1281 tgcgcctcagctgaaagaaacacacacacacacacacacacacacacacacacacac 1340
DB 958 ctgccattgtgcgaacaaacacacacacacacacacacacacacacacacacacacac 1017

```

```

QY 1341 gacgtaagttgagctcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1400
DB 1018 cggcagaccccgcaaaagggctgacgacgattgtgtaaacgacgacgacgacgacgac 1068
QY 1401 attcacccttgaaatcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1460
DB 1069 atttcaccccgcaaaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1128
QY 1461 actgtgtatcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1520
DB 1129 acctgtgacgcttgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1185
QY 1521 acgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1580
DB 1186 aacgctgacgcttgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1245
QY 1581 atgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1640
DB 1246 gtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1305
QY 1641 tgcgacacacacacacacacacacacacacacacacacacacacacacacacacac 1700
DB 1306 tttagcattgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1365
QY 1701 gttgtgttcaacacacacacacacacacacacacacacacacacacacacacacac 1760
DB 1366 gtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1425
QY 1761 ccagaaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1820
DB 1426 ttgactgacgacgacacacacacacacacacacacacacacacacacacacacac 1485
QY 1821 atcaaatcggtagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1880
DB 1486 attacgagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1545
QY 1881 gcatatccttgagcctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1940
DB 1546 tccatgagacgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1605
QY 1941 ccaacacacacacacacacacacacacacacacacacacacacacacacacacac 2000
DB 1606 cccagacatcaaacctgcagacacacacacacacacacacacacacacacacacac 1665
QY 2001 gttgagagagtagagcagatgacacacacacacacacacacacacacacacacac 2042
DB 1666 agcgcagcgcgtatgagatgacacacacacacacacacacacacacacacacacac 1707

RESULT 8
ECOP0XB6 1719 bp DNA BCT 05-OCT-1995
LOCUS Escherichia coli (mutant poxB6) pyruvate oxidase (poxB) gene,
DEFINITION complete cds.
ACCESSION L47693
VERSION L47693.1 GI:1009036
KEYWORDS alpha-peptide; flavoprotein dehydrogenase; poxB gene; pyruvate
oxidase.
SOURCE Escherichia coli (strain K-12) DNA.
ORGANISM Escherichia coli
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
REFERENCE 1 (bases 1 to 1719)
AUTHORS Grabau, C., Chang, X.Y. and Cronan, J.E. Jr.
TITLE Lipid binding by Escherichia coli pyruvate oxidase is disrupted by
small alterations of the carboxyl-terminal region
JOURNAL J. Biol. Chem. 264 (21), 12510-12519 (1989)
MEDLINE 89308683
FEATURES
location/Qualifiers
1..1719
/organism="Escherichia coli"
/db_xref="taxon:562"

```

```
gene
1..1647
/ gene="poxB"
1..1647
/ gene="poxB"
/ note="truncated"
/ codon_start=1
/ transl_table=11
/ product="pyruvate oxidase"
/ protein_id="AAB59107.1"
/ db_xref="GI:1009037"
/ translation="MKOTVAAYIKTLESAGVKRIMVGTGDSLNGLSDSLRMSTIEM
MSTRHEVVAAPAGAEALQSELVACSGCPGNHLINLFDCHRHNVPLVLAHL
PSSISGYSYQETHPOELFRCSSHVCESLSPEDLPOLVLAJMRKAVLNKSVVLE
GDVALKAPRATMHWYHAPQVPTPEEELRLKLAQLIRSSNIALMGSCAGANKE
LVEPAGIKAPIVIALRKHEVENDYDMGTGLIESSGFHMMNADITVLIGTOF
PYRPFYPTDKITIDINPASIGHSKVDNALVDISTRLALLPIVEKRDRELDK
ALDEYRARKSLDLAKRSEKIHPOYLAHEISFADDAFTCDVSTPYMARLYK
MNGRRLLGSNHSNANMPHVGADTEPEROVVAMCGDGGGSLMGDFLSVOMK
LPVKIVFNNSVILGFVAMEMKAGYITDGLHMDINPARIAEACGITGIRVEKASEVD
EALQRAFSIGSPVLVDVVAKEELAIIPQIKLEQAKGFSL"
variation
1647
/ gene="poxB"
/ note="mutant poxB: Tyr-549 ---> Stop"
/ replace="t"
BASE COUNT      419 a      446 c      483 g      371 t
ORIGIN
Query Match      14.0%; Score 302; DB 2; Length 1719;
Best Local Similarity 50.6%; Pred. No. 2,1e-69;
Matches 871; Conservative 0; Mismatches 830; Indels 21; Gaps 5;
327 atgacacacagctacgaacaaatlaattgacacttgaagctcaaggtgtgaagcga 386
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1 ATGAACAACAAGCGTTGCGCTTATATCGCCAAACACTCGAATCGGCGAGGCTGAACGC 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
387 attatggttgggtgtgacagccttaa---tccgatactgtgatactgtccgcaatca 443
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
61 ATCTGGGAGTGCACAGCGACTCTGAACGGCTTAGACAGTCTTAATCGATGAGGCG 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
444 gatattggtgtgtgacagcttcgaataatgaagcggcggttgcagcggtgtgaa 503
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
121 ACCATCGAGTGGATGTCACCGCCGACGAGAAAGTGGCGCTTGGCGCTGGCCCTGA 180
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
504 tcatgtacacacgtggaagctgacatgctgtctgtgtgtgtccctggaaacacac 563
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
181 GCACACTTACGGGAGACTGGCGGTCTGCCGAGATCGTGGCGCCCGGCAACTGACAC 240
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
564 ctgattcaggtcttattgattcgatcgaaatgtgtcgaaaggtgttgccatcgtagc 623
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
241 TTAATCAACGGCGCTGTGATGTCACCGCAATACGTTCCGCTACTGGCGATTGCGCT 300
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
624 catattcgaagtgcccaattgtgtcgagcgttcttcaggaaagcacaacggagatttg 683
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
301 CATATTCCCTCCAGGGAATTTGGACGCGCTATTTCACGGAACCCACCCACAAGACTA 360
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
684 tllaagaatgtctgtgttactgtacgtgaaatgtgtgtgtgtgtgtgtgtgtgtgtgt 743
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
361 TTCGCCGATGTAGTACTATTGCGAGCTGTTTCCAGCCCGGACAGATGCCACAAGTA 420
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
744 ttgcatacgcgattcgtacccaatgtgcggtgaaggtgtgtgtgtgtgtgtgtgtgt 803
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
421 CTGGGATTTGGCATGCGAAGGCGGTGCTTAACCGTGGCGTTCGTTGCTGTGTACCA 480
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
864 ggtgatattcgttaagaagaagcaggtgaagttacttacttcaattcactatctctct 863
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
481 GGGCGAGGGGCTTAAACCTGCGCAGAAAGGGGC---AACCATCCACTGGTATATGCG 537
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
864 ggcactctgtgtgttcccgatctactaagctgacgctgtgtgtgaagcgttactaac 923
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
538 CCACACACAGTGTGACGCGGGAAGAAGAGTTACGCAAACTGGCGCACTGTGTGCGT 597
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
924 aagcctaagctgtcacttgttctgtcggtgcggtgtgaagaatgtctgcgcgaggtg 983
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```

||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
598 TATTCACCAATATCCGCTGATGTGTGACAGCCGCTCCGCGGGCCCATAAAGATTAA 657
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
984 ttgaggtgtgaggaagaattaaatcacccgattcggtgtgtgtgtgtgtgtgtgtgtgt 1043
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
658 GTTGAGTTTGGCGGGAATTAAGCGCTATGTTGTCATGCGCTCGGCGTAAGACATAT 717
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1044 atccagcatgaaacccgtttgaggttcgcatgtctgtgctgtgtgtgtgtgtgtgtgtgt 1103
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
748 GTTCGATATGATATATCCGATATGTTGGAAATGACCGGGGTTAATGCGGTTCGTCAG 777
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1104 gtgattgtgtccaatatgagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1163
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
778 TTCCATACCATGATGATGAGCCGACACAGTTAGTGTACCTGCGACCAATTTCCATCCG 837
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1164 gatttcttctc---aagacacagttgcccaggtgtgtgtgtgtgtgtgtgtgtgtgtgt 1220
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
838 GCTTCTACCCGACCGCATGCGCAAAATCATTCAGATTGATATCAACCCAGCCAGCTCCG 897
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1221 cgaagtacacaggtgaagatctccgtgtgaacggtgtgtgtgtgtgtgtgtgtgtgtgt 1280
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
898 GCTCACACGAGGTGATATGCTGCTGCGGCGATATCAAGTGCACCTGGTGCATTG 957
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1281 ttgctctatgtgaagaaacacagatgttcttcttcttcttcttcttcttcttcttctt 1340
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
958 CTTCATTGTGTGAGAAAGAAAGCCGATGCAAGTTCTGTGATTAAGCCCTGGAAGATTAC 1017
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1341 gagcgttaagtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1400
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1018 CGCGACGCCCGCAAGCGGTGACGATTTAGCTTAACCGAGCG-----AGAAAGCC 1068
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1401 attacacctgaatacgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1460
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1069 ATTACCGGCATATCTGCGCGACGAAATTAATGATTTTGGCGGAGTAGCGCTATTTC 1128
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1461 actgtgtatcccgcatgtgcaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1520
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1129 ACCTGTGACGTTGTGATGCGCAACGGGTGTGGCGGACGCTTATCT---AAAAATGAACG 1185
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1521 acggtgagcttgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1580
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1186 AAGCGTCCGCTGTAGTGTGCTTTAAACGAGGTTGATGAGCTTAACGCCATGCGCACG 1245
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1581 attgtgtcgaaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1640
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1246 GTGGGTGGGACAGGACAGAGCCAGACAGTCAAGTCAAGTGTGGCGGATGCGCGGT 1305
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1641 ttggtcattgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1700
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1306 TTATACATGTTGATGGGGAATTTCTCTCAGTACGACAGATGAACCTGCACGTGAATTT 1365
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1701 gtgtgtttaaacaagcttctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1760
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1366 GTGCTCTTAAACAACGCTGCTGGGCTTTTGTGGGATGTGAGATGAAGCTGTGTGTAT 1425
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1761 ccaagaattgttactgacatgaagaaatgaatttcgaagagattgtgtgtgtgtgtgtgt 1820
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1426 TTGACTGACGGCAGCAGACTACACAGCAACAACTTTGCCCGCATGCGGAACGTGGCG 1485
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1821 atcaaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1880
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1486 ATTACGGGTATCGCTGTGAAAAAGCGTGTGAAGTTGATGAAGCCCTGCAACGCGCTTC 1545
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1881 gataatcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1940
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1546 TCCATCGACGGTCCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1605
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1941 ccaaccatcagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2000
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1606 CCGCAGATCAAACTCGAAGGCGCAAGGTTTACGCTGTAAATCTGCGGCATATTC 1665
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2001 gttgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2042
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```


QY	1641	ttggcgcgtcgcgcgtgggagagctcttcgaccgttaagctctgcaccaccttcgcgtgaagct	1700
QY	1701	gtgagctttaacaacagctctcttgggcaatgagagctcttgagagctgcgttgagagacag	1760
Db	1306	ttttacatgctgattggggcgattttccctctcagtagtgcacatgacaaactgcagtaaaatt	1365
QY	1366	gttcgcttttaacacacagcgctgctggagctttgttggcgatgtgaatgaaactggtggctat	1425
QY	1761	ccagaatttgctactgcagcatgagaaagtgaatttcgcagagatcttgaggcgctgcggt	1820
Db	1426	ttgactgcacggcaccgaaactacacagacacaaactttggcccgatgtcccaacgctggcgc	1485
QY	1821	atcaaatcgtgaacgcatcaacgcagtcggaagaatttcggagacagctagctgaagcatg	1880
Db	1486	atttaccggtatccgtctgacaaaaaacgcgtctgaaattgataaagcccttcgaacgctcttc	1545
QY	1881	gcatalccctgagacctgctactgatacgcatacgcaggaatcctaattgcgtctgcatacca	1940
Db	1546	ttccatgcacgggtccggtgtgttggtgatgtggtgtgcgcacaaagaagatgttagcatatcca	1605
QY	1941	ccaaccatcaagtgtggaacaggtcatatggtatccagcaagaagcgcgccacccgaacgctctt	2000
Db	1606	ccgcagatcaaaactgcgaacagcgcacaaagctttcacacctgtatatgtcgtgcgcacatcatc	1665
QY	2001	ggtgagagtagtagagcgatgcatgcactgcggccgcttgcac	2042
Db	1666	agcgcacgcggtgatgactgattccaaactgcgcgaacaaacaaac	1707
RESULT 10			
ECOP0XB14G			
LOCUS	ECOPOXB14G	1719 bp	DNA
DEFINITION	Escherichia coli (mutant poxb14) pyruvate oxidase (poxb) gene, complete cds.		
ACCESSION	L47690		
VERSION	L47690.1	GI:1009030	
KEYWORDS	alpha-peptide; flavoprotein dehydrogenase; poxb gene; pyruvate oxidase.		
SOURCE	Escherichia coli (strain K-12) DNA.		
ORGANISM	Escherichia coli		
	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia.		
REFERENCE	1 (bases 1 to 1719)		
AUTHORS	Grabau, C., Chang, Y. Y., and Cronan, J. E., Jr.		
TITLE	Lipid binding by Escherichia coli pyruvate oxidase is disrupted by small alterations of the carboxyl-terminal region		
JOURNAL	J. Biol. Chem. 264 (21), 12510-12519 (1989)		
MEDLINE	89308683		
FEATURES			
source	location/Qualifiers		
	1..1719		
gene	/organism="Escherichia coli"		
	/strain="K-12"		
	/db_xref="taxon:562"		
	1..1719		
	/gene="poxb"		
	1..1719		
	/gene="poxb"		
	/codon_start=1		
	/trans_table=1		
	/product="pyruvate oxidase"		
	/protein_id="AAB59104.1"		
	/db_xref="GI:1009031"		
	/translation="MKQTVAVIAKTIETSAQVIRKMGVYGGSLNGISLSTIRMGIEH MSTRHEVAAPAAACAEKQLSSELAIVCACSGCPGNLHNLINGIPDCHRNHVPVLAIAAH PSSISGSGYFQETPEQELFRECSHYCELVSSPEQIPVLAIAKRAVNAIRSVVLAIAH GDVALKPAPEGATMHWYHAPQPVPTPEEELRLAQLRGSNTIALMGSCAGAKHK LVEAGKIKAPITVAHLRGKEHEVDNPDVMTGLIGSSFHFMAMNDLTLLSTQST PYRFVYPRDAKLTIOIDINPASIGASHKSDMALVQGIKSTLRALLPIVERKADRKIDM ALDEYPRARGLDILAKPSEKAHPRVYLAHRTSHFAADALFTCDVGPPIYMAARYL MNGKRLIGSNHSCMANMHPYGAQATEPEROVAMCGDGGGFSMLGDFLTVQOM LPNVIVFNNSVLIFVAMEMKAGVLTIDGELIDNFRALIEAGGITGIIVKESAEV EALORASISDGPVLVDVVAKEELAIPQILDEQAKGFSLYMLRVITSGRDEVELTALA		

[illegible]

OY	444	gaatttgagtgaggcaacgttcgaaatggaagcgaggcggtcttgcagccggtgagaa	503
Db	121	ACCATCGATGATGATTCACCCCGCACGAAGAAGTGGCGCCTTTGCGCTGGCTGAA	180
OY	504	tcgtatgaactctggggagctcgcaatgtagtgcgtctcttggtctcttgaaacacac	563
Db	181	GCACACATTACCGGAGAACTGGCGGTGGCGCGGATCGTGGCGCCCGCAACTGCAC	240
OY	564	ctgagtcgaaggctcttaatgaltcgacatcgaaatggtgcgaagggtgtgtgcatac	623
Db	241	TTTAATCAACCGCGCTTTCGATTCGCACACCCCAATCAGCTTCCGGTACTGCGAT	300
OY	624	catattccgagtgcccgcaatttgtttcgaagctcttcacgaagaacgcataccgaatt	683
Db	301	CATATTCCCTCCACCGAATTTGGCAGCGCGCTATTTCAGAGAAACCCACCCACMA	360
OY	684	cttaagaagaatcctctgtttctatctcgagaatgtgaatggtggtgagagaggtaga	743
Db	361	TTCCCGCAATGTAACTACTATTGGAGACTGCTTTCCAGCCCGGAGCAGATCCCA	420
OY	744	ctgacatcaacggaaltcgactcacacatgagcggtgaaaggtgtgtgcgtatgata	803
Db	421	CTGGCGATTTGGCATTCGCCCAAAAGGGGTGCTTAACCGTGGGTTTCGGTTCGT	480
OY	804	gggtatataatcgctaaagaaagcaagctgacggtacttataatccaatltctcttc	863
Db	481	GGCGACGTGGGCTTMAAACCTGGCGCACGAAGGGGC--AACCATGCAGCTGAT	537
OY	864	ggaaactcctgtggtctcccggaatccctacatgagctcgcaagcgtgtgtgaaagc	923
Db	538	CCACACACAGTCGAGACCGCGGAAGAAGAGATTACGCAAACTGGCGCACTGTG	597
OY	924	aaagctaagctctgcaactctgtctcgcgtgagcggtgaaagatgctgcgcgagag	983
Db	598	TATTCCAGCAATATTCGCCGCTGATGTGTGGACGGCTGGCGCGCGCATTAAGA	657
OY	984	cttgagctgtgcggaagaatlaaaatcaacgcatctgggcatgctgcgtgtgtgaag	1043
Db	658	GTTTACGTTTGGCGGGAATAATTAAGGCGCTATTGTTCAATGCCCTGGCGGT	717
OY	1044	atcagaagaatgaaatccgcttgagggtcgcgcatgtctgcgcctctgtgttaagcg	1103
Db	718	GTCGAATACGATTAATCCGTAATGATGTGGAATACCGGGTTAATGGGCTTCGT	777
OY	1104	gctgagatcgctccaaatggagggcggaatcgcgtaattctatcttggtgaagatlt	1163
Db	778	TTTCATACGATGATGAAACGCCCGACAGCTTAAGTGTCTACTGCGACGCCAT	837
OY	1164	gatttccctccta--aagacaaactgtccacagtgagatatacaacggtgcagata	1220
Db	838	GCTTTTACCGGACCGATGTGCCAATATCATTTAGATTTGATATCACCGACG	897
OY	1221	cgaaatcaccagtggaagtatccggtggaacgggtgtagtgtgtcgtgcaacaatc	1280
Db	898	GCTTACAGCAAGGTGATATGACACTGTGTCGGGATATACATGACACTGTGTC	957
OY	1281	ctgctctcaatggaaggaanaaacagatctctctctcttgatctcgabctctaaag	1340
Db	958	CTTTCATTTGGTGCAGCAAAAAGCCCGATTGCAACTTTCTGTGATTAAGCCG	1017
OY	1341	gagcgtaatgtgagctctgcgtgtgtagagagctatacacataaagctcgagaag	1400
Db	1018	CGCGACGCCGCAAAAGGGCTGGACGATTAAGTAAACGAGG-----AGAA	1068
OY	1401	atcaaccctgataatcgtctctctatcttggaaacgagctgtgcgtgataagata	1460
Db	1069	ATTTCACCGCAATATTCGCGCGCACGAATAATTAGTCATTTTGGCCGCGAT	1128
OY	1461	acgtgagataccggcagatgtgcaatgtgtgtgcaatgagaggtatacatgagaat	1520
Db	1129	ACCTGTACCGTTGTACGCCCAACGGGTGTGGCGCGCACGTTATCT--AAAA	1185

QY	1521	aacgggaactcttgtaggttcaattccgcaacggcaagatgacaaagctgtcccaatgacg	1580
Db	1186	AAGCGTGGCTGTAGAGTTGCTTTAAACCAAGCTTGATGAGCTAACGCCATGCGCAGGC	1245
QY	1581	atttgtagcaaaagtgctgatacgaaacccgacagtgatccgcatgtgtggagatggtgtc	1640
Db	1246	GTGGGTGCGGAGGCGAACAAGACCCAGAACCTCAGGTGTGTGCCATGTGGCGCGATGGCGT	1305
QY	1641	ctgggaatgcgtctgggtggaggtctctgacccgttaagctgtgacaaattccgctgaaggtc	1700
Db	1306	TTTAGCATGTGTGATGGGCGGATTTTCCCTCATGATGTCAGATGAACCTCCAGTGAAATT	1365
QY	1701	gtgtgtgtttaacaacacgtctctctgtggacatggtgtgaagctgtggagatgctgtgtggagacg	1760
Db	1366	GTCTGCTTTTAAACAACGCGTGGGCGCTTTGTGGCGATGGAGATMAAGCTGTGGGCTAT	1425
QY	1761	ccgaatatttgtaactaaccttgagagagaaatttcgcagaagatgtgscggctctggggtc	1820
Db	1426	TTTGACTGACGGCACCCGAACTACACGACACAACTTTGCCCGCATGGCGAAGCCTGGCGC	1485
QY	1821	atcaaatcgttacgaataccgaatccgagaagaattctgcgacagctagctgtgaggaattg	1880
Db	1486	ATTACGGGTTTCCGTGTAGAAAAGCGTTGTGAAGTTGATGAAGCCCTTCAACGGCCTTC	1545
QY	1881	gcatatcctggaacctgtactgatacgatatactgcgaacggaatccctaattgctgtcgatccca	1940
Db	1546	TCATCTCAGCGTCCGGGTGTTGGTGATGTGGTGTCGGCCAAAGAAAGATTAGCCATTCCA	1605
QY	1941	ccaacatacagctgaggaaacaggtatcagggaattcagaagaagcgccacccgaacacgctctc	2000
Db	1606	CCGCGATCAAACTCCAAACAGGCCCAAGGTTTCAACCTGTATATCTCGCGCAATATC	1665
QY	2001	ggtggagagatbaagacgaatgcatactctggcccgctcgaaac	2042
Db	1666	AGCGAGCGCGTGATGAAGTGATCTTAACGTGGGGAACCAAC	1707

```

RESULT 13
ECOP0XB16G
LOCUS      ECOP0XB16G      1719 bp      DNA      BCT      05-OCT-1995
DEFINITION Escherichia coli (mutant poxb16) pyruvate oxidase (poxb) gene,
ACCESSION complete cds.
VERSION    LA7692
KEYWORDS   LA7692.1 GI:1009034
           alpha-peptidase; flavoprotein dehydrogenase; poxb gene; pyruvate
           oxidase.
SOURCE     Escherichia coli (straln K-12) DNA.
ORGANISM   Escherichia coli
            Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
            Escherichia.
REFERENCE  1 (bases 1 to 1719)
            Grabau, C., Chang, Y.Y. and Cronan, J.E. Jr.
            Lipid binding by Escherichia coli pyruvate oxidase is disrupted by
            small alterations of the carboxyl-terminal region
            J. Biol. Chem. 264 (21), 12510-12519 (1989)
            89308683

FEATURES
    source          location/qualifiers
    1..1719
    /organism="Escherichia coli"
    /straln="K-12"
    /db_xref="taxon:562"
    1..1719
    /gene="poxb"
    1..1719
    /gene="poxB"
    /codon_start=1
    /transl_table=1
    /product="pyruvate oxidase"
    /protein_id="AAB59106.1"
    /db_xref="GI:1009035"
    /translation="MKQTVAAYIAKTLSSAGYRKMGVDSGLNSLSDSLNRMTIEK
    MSRRHEVAFAPAGAEKALGSEGLAVACGSGCPGLHLINGLPDCRHNRHVPVLAIAHT
    PSSIEISGIFQETHPELIFRECSHYCELVSSPEIIPVLAIAMKRAVLNKGVSVVLP"

```


AUTHORS
Stover, C. K., Pham, X. Q., Erwin, A. L., Mizoguchi, S. D., Warrenner, P., Hickey, M. J., Brinkman, F. S., Hutnagle, W. O., Kowalik, D. J., Lagrou, M., Garber, R. L., Goltz, L., Tolentino, E., Westbrock-Wadman, S., Yuan, Y., Brody, L. L., Coulter, S. N., Folger, K. R., Kas, A., Larbig, K., Lim, R., Smith, K., Spencer, D., Wong, G. K., Wu, Z. and Paulsen, I. T.
Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen
NATURE 406 (6799), 959-964 (2000)

JOURNAL
MEDLINE
REFERENCE
AUTHORS
2 (bases 1 to 10977)
Stover, C. K., Pham, X. Q., Erwin, A. L., Mizoguchi, S. D., Warrenner, P., Hickey, M. J., Brinkman, F. S., Hutnagle, W. O., Kowalik, D. J., Lagrou, M., Garber, R. L., Goltz, L., Tolentino, E., Westbrock-Wadman, S., Yuan, Y., Brody, L. L., Coulter, S. N., Folger, K. R., Kas, A., Larbig, K., Lim, R., Smith, K. A., Spencer, D. H., Wong, G. K., Wu, Z., Paulsen, I. T., Reizer, J., Salier, M. H., Hancock, R. E. W., Lory, S. and Olson, M. V.
Direct Submission
Submitted (16-May-2000) Department of Medicine and Genetics, University of Washington Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA
Location/Qualifiers
1. 10977
/organism="Pseudomonas aeruginosa"
/strain="PA01"
/db_xref="taxon:287"
complement(106..1023)
/gene="PA5293"
complement(106..1023)
/gene="PA5293"
/codon_start=1
/transl_table=11
/product="probable transcriptional regulator"
/protein_id="AAG08678.1"
/db_xref="GI:9951608"
/translation="MTRRLPPVLAALFAEAAHASTFRAGEELAITQSASVRIHRL EHHGCRLEFHHGRQQLDTEPARLLGLNDGEPALREACTALVDDATRLKAPSTL TLRMLPRLSRFDLPNDIVOLTSAMVDSDVDFOREPDCAVILGSGSPWETA ALFAEMLVPCDDEAVEPWLRLRDLSELIHPDPRDRMRRLORTGLGEVSLKGA QVEDTLELGIYAARGVSGIDGVVAEVAOGRIGLPPMVAAVASESHLVMPRAR RGEORFQRLDPLLAEVAAHRLPVERLA"
1172..2638
/gene="PA5294"
1172..2638
/gene="PA5294"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="AAG08679.1"
/db_xref="GI:9951609"
/translation="MSSPSLVELKAILRLAGPLIAOQAVAVAFDTVMKLGPPDA LAAGGCAVYAEVSTFCVVAAGNLVAIRHCCDDAAGAAAARSGLWGAALALA AGLLWMLRPLLVFGQAPQTVGAMGFLSHTEPALRGVMAFWLREGTSADGAGV MAISVIGALANLANISFTIGLCPRLGAGIGIYALVNMNCPILLALYIRIOPY AERTSLRGICRPOKAWETLRLGLPIGGTYAVESGMFTVATLGMGILGHAIHAHOT AIDAVYAEFWPGLSATYTRIGQHPAGARLLEARRAGRVGIGFGALCMILPAGLFW MMEBAITIGLELDRDAPANREVAAMAVSILAIAAFELFDGTQNVAMGAILKLAFT FLVIGACYMLVGLACILAFAGMGAGVMMGLAGLACAAIGLTFLAFEMKTRALLP KATASEASALNCAGAGSARLCPGNAPVPTAAD"
complement(2550..4226)
/gene="PA5295"
complement(2550..4226)
/gene="PA5295"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="AAG08680.1"
/db_xref="GI:9951610"
/translation="MSAPAEPLRLILLADTPDPAWPLGERLRALGPAFSLSYTTWEG AATLFAEPREGILLATPACPLGTPCPWVILLQOPPAQVGVVMDLAEOUSDS LRRCRYARELIGIATLLOLLADODPOTLIGANROGROTLLAARSEFDGIVGHD LDNFRVYVNDISLGGDRILLIOVNNLRGFMENGDLSARIGSEFALLDTRDPCA ERVARIVECLGEPTWIDGSLILGSLGLAHARADGADPLMMHATIAQOAKSROG

CTFHEVDRLNRGVSADLAEELRLARLREDELHAYOPRICLDSGRIVGLAELVNR HGEHGLPTSEFVLAESGLIYGLGVIALRALRDMQWLGRLGLHMAVNSFQ FOSGLPTLORLLEEKGVDARLFELETETAVARSDVOYLOTOALGOIGVRSLD FGTESSFVHNSIPITLLKIDRSFVGMOORAPNOLVAMINILANINIEVAEVS ETLQOQOLRFGCDQVGVWISPPFLAELARLIGERSAHNGPFLNG"
4414..6423
/gene="rep"
/note="PA5296"
4414..6423
/gene="rep"
/codon_start=1
/transl_table=11
/product="ATP-dependent DNA helicase Rep"
/protein_id="AAG08681.1"
/db_xref="GI:9951611"
/translation="MSRLNPOQAVVWGGPILVLAGSGKTSVTRKTAIVVOC GTRQIVYVFTFKARBEKERVGTLLRGESEGLVSTFPHNLGILITKEHRLRT KPGSIFDESQIKALTDIMOKEYSGDGVDEKNTYIGAMKNDLILPEALEKARK EOTPAIVLYHQRTRLAVNAVDFDILLQPVKLEBHPDYLOKQNVRYMLVDEXD TMAQYLLVLLKLVRAQFVYVGDQDSIYAMRGARPENIMQLKEDPSLKVMLEGN YRSRLIKCANVLIANNPVEFKOLSEMGHGPPIRVIRRNDAEARIAMLTIL HTRPERSEKALIRGNHOAKIMELKLOHNOTPRLSGTSPFSGRQEVDMGYRFL LVNPDNDNAFLRVINVRREIGSKTEKLGNYATQRTISMTACDNGELAHDSRFH ERLQRFKRMWDGIRQCAENEPJAVLSWMDIDYENWLQNASDQVAAEFKSNVNF LIEALKNTLREDEGDMTIDQATIKVLRMLEROQEEEGAGGVMMTTHASGLFF PYVFIQMEEEIILPHRSSIRADYVEERRLAAYVITPARONLAWTFAAKKROYCEIID CSPSRFLDEPDLLEWEGMEDAPQEVKAKKANALADIRMLKR"
6557..8275
/gene="poxB"
/note="PA5297"
6557..8275
/gene="poxB"
/codon_start=1
/transl_table=11
/product="pyruvate dehydrogenase (cytochrome)"
/protein_id="AAG08682.1"
/db_xref="GI:9951612"
/translation="MSSKRYAEIVETLEAGVHRCYGIYDGLNHYTDAIHSQLOM VHVHEEAAFAAAEASYIGRLTACGSGSPGLHFINVEKORRARPVILASOI VTPOIGMEFQEVDFKAVVASCVFCSGPEGARVRVVALACQALNRGAVNVLIP ADISQATKNDIPESVHPQPVLRSPSAPLODVARLHAHKKITGYSCQGHADL VALADRLKAPLAHTSRKADYEVDNPNMGKTMGLTGESGHMMTECDTLLGLGADA WAOYYPQKATLIDVDRGSHLGRHPIDLVSGCVITPLEALLPLEARERSFLDC LEHRESRILTEKEEOAGKGLTHPQNLIDLOHASBDAFTADGASAWVLRHLIH SNGKRRITLSLVHGTMANAMPQALGKAYPEROYVITSDDGILGLDLTAIQCK LPIKVVYVNNASLNFVELOKVEGLINDYLDLPDARLAEVIGFGRVYTRSEE AAVQEFIAQPGPALDVHTNPALVMPKLTIEFGVADTALYAKAVLSGFKOVETLL VNNLKR"
8404..8976
/gene="PA5298"
8404..8976
/gene="PA5298"
/codon_start=1
/transl_table=11
/product="xanthine phosphoribosyl transferase"
/protein_id="AAG08683.1"
/db_xref="GI:9951613"
/translation="MDILKDKIRSEGIIVLSEHYLVKDAFLNHQIDPOLMOOVGHAF RFRQGITKIVTIEASGIRAPVAMAGLGVPIFAKRYOSTLTIDNLTYSKVSFTQO TESTIATSAKHLNADHVLVYIDDFLANGHAAKALIDLIGAGASINAGLGVITKSFOD GRALLESSEGRVESLARVKSLAGGVVEFLD"
complement(8984..10843)
/gene="PA5299"
complement(8984..10843)
/gene="PA5299"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="AAG08684.1"
/db_xref="GI:9951614"
/translation="MGPIGIGKPNRLVNLAYORLTPPEROLITVYALSIPRAGG DIORRFLPEPAERVFADYBELDILHARRELPANRIVEEFTYLOPGLDLSAPAOQY ISCNYSHVARDINAKGVNAVAQIVARHPRPGKLSACNDPITLIDLLPMLKRRAGE

BASE COUNT 1897 a 3798 c 3545 g 1737 t

This Page Blank (uspto)